

Fig. 1

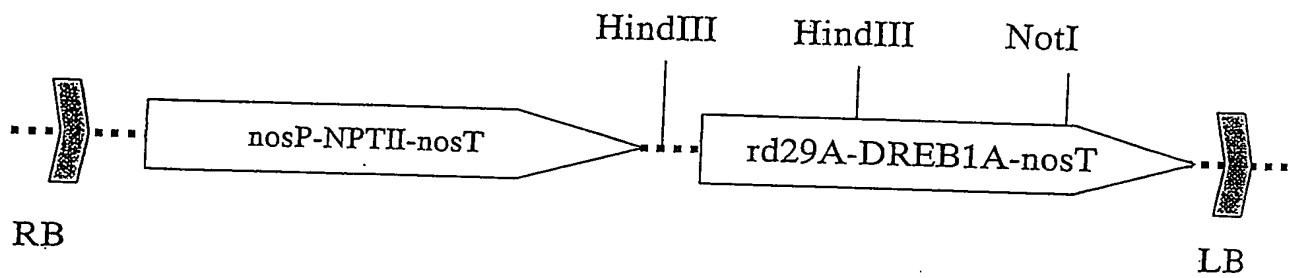


Fig. 2-1

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Sequence 1      : DREB1A.nuc
Size           : 651
Matching Position : 1 - 651

Sequence 2      : DREB1B.nuc
Size           : 642
Matching Position : 1 - 642

Matching Condition.

Matches        : -1
Mismatch       : 1
Gaps           : 1
*N+            : 2

Matching       : 85.04 [%]
Weight        : -451

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC
***** **** ***** ***** ***** ***** **
1 : ATGAACTCAT TTTGAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAG-- -----CC

61 : TC-AGGCGGT GATTATATTC CGACGCTTGC GAGCAGCTGC CCAAGAAAC CGGCGGGTCC
** ***** ** ***** * ** * ** ***** **
51 : TCAAGGCGGA GATTATTGC CGACGTTGGC CACGAGTTGT CCAAGAAAC CGGCGGGCCG

120 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT ATACAGAGGA GTTCGTCCGA GAAACTCCGG
***** ***** ***** ***** ***** * *****
111 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAA GAAACTCCGG

180 : TAAGTGGGTT TGTGAGGTTA GAGAACCAA CAAGAAAACA AGGATTGGC TCGGAACATT
***** * ** * ** ***** ***** ***** **
171 : TAAGTGGGTT TCTGAAGTGA GAGAGCCAA CAAGAAAACC AGGATTGGC TCGGGACTTT

240 : TCAAACCGCT GAGATGGCAG CTCGAGCTCA CGACGTTGCC GCTTTAGCCC TTCGTGGCCG
***** ***** **** ***** ** ** ***** * *****
231 : CCAAACCGCT GAGATGGCAG CTCGTGCTCA CGACGTCGCT GCATTAGCCC TCCGTGGCCG

300 : ATCAGCCTGT CTCAATTTTC CTGACTCGGC TTGGAGACTC CGAATCCCGG AATCAACTTG
***** ** ***** ***** ***** * ** ***** * *****
291 : ATCAGCATGT CTCAACTTTC CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAACATG

360 : CGCTAAGGAC ATCCAAAAGG CGGCGGCTGA AGCTGCGTTG GCGTTTCAGG ATGAGATGTG
*** ***** ***** * **** ***** ** ***** * *****
351 : CGCCAAGGAT ATCCAAAAG CGGCTGCTGA AGCGGCGTTG GCTTTTCAAG ATGAGACGTG

420 : TGATGCGACG ---ACGGATC ATGGCTTCCA CATGGAGGAG ACGTTGGTGG AGGCTATTTA
**** ***** *** ** ***** * ** ***** * *****
411 : TGATACGACG ACCACGAATC ATGGCCTGGA CATGGAGGAG ACGATGGTGG AAGCTATTTA

477 : CACGCGGAA CAGAGCGAA ATGCGTTTTA TATGCAGAT GAGCGGATGT TTGAGATGCC
** ***** ***** ***** ***** * ** * ** * **
471 : TACACCGAA CAGAGCGAAG GTGCGTTTTA TATGGATGAG GAGACAATGT TTGGGATGCC

537 : GAGTTTGTG GCTAATATGG CAGAAGGAT GCTTTTGCCG CTTCCGTCCG TACAGTGAA
** ***** * ***** * ***** ** ***** * ** *****
531 : GACTTTGTG GATAATATGG CTGAAGGCAT GCTTTTACCG CCGCCGCTG TTCAATGAA

597 : TCATAATCAT GAAGTCGACG GCGATGATGA CGACGTATCG TTATGGAGTT ATTAA
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Fig. 2-2

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591 : TCATAATTAT GACGGCGAAG GAGATGGT-- -GACGTGTG CTTTGGAGTT ACTAA

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Sequence 1 : DREB1A.nuc  
 Size : 651  
 Matching Position : 1 - 651

Sequence 2 : DREB1C.nuc  
 Size : 651  
 Matching Position : 1 - 651

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2

Matching : 86.70 [%]  
 Weight : -476

1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTCC  
 \*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\* \* \*\*\*\*\*  
 1 : ATGAACTCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC

61 : TCAGGCGGTG ATTATATTCC GACGCTTGCG AGCAGCTGCC CCAAGAAACC GGCGGGTCTG  
 \*\*\*\*\*  
 61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATA TACAGAGGAG TTCGTGCGAG AAACCTCCGGT  
 \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAACCTCCGGT

181 : AAGTGGGTTT GTGAGGTTAG AGAACCAAAC AAGAAAACAA GGATTGCGCT CGGAACATTT  
 \*\*\*\*\*  
 181 : AAGTGGGTTT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGCGCT CGGGACTTTC

241 : CAAACCGCTG AGATGGCAGC TCGAGCTCAC GACGTTGCCG CTTTAGCCCT TCGTGGCCGA  
 \*\*\*\*\* \*\*\*\*\*  
 241 : CAAACCGCTG AGATGGCAGC TCGTGTCTAC GACGTCGCCG CCATAGCTCT CCGTGGCAGA

301 : TCAGCCTGTC TCAATTTTCG TGACTCGGCT TGGAGACTCC GAATCCCGGA ATCAACTTGC  
 \*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 301 : TCTGCCTGTC TCAATTTTCG TGACTCGGCT TGGCGGCTAC GAATCCCGGA ATCAACTGCT

361 : GCTAAGGACA TCCAAAAGGC GGCGGCTGAA GCTGCGTTGG CGTTTCAGGA TGAGATGTGT  
 \*\* \*\*\*\*\*  
 361 : GCCAAGGAAA TCCAAAAGGC GGCGGCTGAA GCCGCGTTGA ATTTTCAAGA TGAGATGTGT

421 : GATGCGACGA CGGA---TCA TGGCTTCGAC ATGGAGGAGA CGTTGGTGA GGCTATTTAC  
 \*\* \*\*\*\*\*  
 421 : CATATGACGA CGGATGCTCA TGGTCTTGAC ATGGAGGAGA CTTTGGTGA GGCTATTTAT

478 : ACGGCGGAAC AGAGCGAAAA TCGTTTTTAT ATGCACGATG AGGCGATGTT TGAGATGCCG  
 \*\*\* \*\*\*\*\*  
 481 : ACGGCGGAAC AGAGCCAAGA TCGTTTTTAT ATGGATGAAG AGGCGATGTT GGGGATGTCT

538 : AGTTTGTGG CTAATATGGC AGAAGGGATG CTTTTCGCCG TTCCGTCCGT ACAGTGAAT  
 \*\*\*\*\*  
 541 : AGTTTGTGG ATAACATGGC CGAAGGGATG CTTTACCGT CGCCGTCCGT TCAATGGAAC

Fig. 2-3

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598 : CATAATCATG AAGTCGACGG CGATGATGAC GACGTATCGT TATGGAGTTA TTAA
      ***** ** * ***** ** ***** ***** ** * ***** ** ****
601 : TATAATTTTG ATGTCGAGGG AGATGAT--- GACGTGTCCT TATGGAGCTA TTAA

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Sequence 1          : DREB1A.nuc
      Size           : 651
      Matching Position : 1 - 651

Sequence 2          : DREB1D.nuc
      Size           : 675
      Matching Position : 1 - 675

Matching Condition.

Matches             : -1
Mismatch            : 1
Gaps                 : 1
#N+                  : 2

Matching             : 68.72 [%]
Weight               : -233

1 : ATGAACTCAT TT---TCTGC TTTTCTGAA ATGTTT----- --GGCTCCGA TTACGAGTCT
      ***** ** * ***** ** ***** ***** ** * *****
1 : ATGAATCCAT TTTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT

52 : TCGGTTTCCT CAGGCGGTGA TTATATTCGG ACGCTTGCGA GCAGCTGCCC CAAGAAACCG
      ***** * ***** * * * * * * * * * * * * * * * * * * * *
61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA

112 : GCGGGTCGTA AGAAGTTTCG TGAGACTCGT CACCCAATAT ACAGAGGAGT TCGTCGGAGA
      ** ** * * ***** ***** ** ** ** * * ***** ***** **
121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG

172 : AACTCCGGTA AGTGGGTTTG TGAGGTTAGA GAACCAAACA AGAAAACAAG GATTTGCTC
      ** ** ***** * ***** ** ** ** * ***** * * ***** *
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAATCTAG GATTGGTTA

232 : GGAACATTTT AAACCGCTGA GATGGCAGCT CGAGCTCAGC ACGTTGCCGC TTTAGCCCTT
      ** ** ***** ** * *** ***** ** ** ***** * * ***** **
241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

292 : CGTGGCCGAT CAGCCTGTCT CAATTTGCTT GACTCGGCTT GGAGACTCCG AATCCCGGAA
      ***** ** * * ***** ***** ** ** ***** ** * ** ** **
301 : CGTGGTCGCT CTGCTTGTCT CAATTTGCTT GATTCTGCTT GCGGCTTCG TATTCTGAG

352 : TCAACTTGCG CTAAGGACAT CCAAAAGGCG GCGGCTGAAG CTGCGTTGGC GTTTCAGGAT
      * ***** ***** ** ** ** ** ** ** ** ***** ***** ***** **
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT

412 : GAGA----- -TGTGTGAT- ----GCGACG ACGGA-TCA- TGGCTTCGAC A-TGGAGGAG
      **** * * *** * ** ***** ** ** * * * * *****
421 : GAGACTACGA CGGAGGGATC TAAACTGCC GCGGAGGCAG AGGAGGCGGC AGGGGAGGGG

457 : ACGTTGGTGG AGGCTATTTA CACGGCGGAA CAGAGCGAAA ATGCGTTTTA TATGCACGAT
      * ** ** ** * * * * * * * * * * * * * * * * * * * *
481 : GTGAGGGAGG GGGAGAGGAG GCGGAGGAG CAGAATGGTG GTGTGTTTTA TATGGATGAT

517 : GAGGCGATGT TTGAGATGCC GAGTTTGTG GCTAATATGG CAGAAGGGAT GCTTTTGCCG
      ***** * * * * ***** * ** ** * ***** * ** *****
541 : GAGGCGCTTT TGGGATGCC CAACTTTTTT GAGAATATGG CGGAGGGGAT GCTTTTGCCG

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Fig. 2-4

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577 : CTTCCGTC CG TACAGTGGAA TCATAATCAT GAAGTCGACG GCGATGATGA CGACGTATCG  
 \* \*\*\* \* \* : \*\*\*\*\* \* \*\* \* \*\*\*\* \* \* \* \* \*\*\*\*\* \*\*  
 601 : CCGCCGGAAG TTGGCTGGAA TCATA---AC GACTTTGACG GAG-TG--GG TGACGTGTCA

637 : TTATGGAGTT -----ATTA A  
 \* \*\*\*\*\* \* \* \*  
 655 : CTCTGGAGTT TTGACGAGTA A

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Sequence 1 : DREB1A.nuc  
 Size : 651  
 Matching Position : 1 - 651

Sequence 2 : DREB1E.nuc  
 Size : 546  
 Matching Position : 1 - 546

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 54.70 [%]  
 Weight : 0

1 : ATGAACATCAT TTTCTGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTC-  
 \*\*\* : \*\*\*\* : \*\*\*\* : \*\* \* \*\*  
 1 : ATG----- ----GAAA-- ----ACGA-- --CGATATCA  
 60 : CTCAGGCGGT GATTATATTC CGACGCTTGC GAGCAGCTGC CCCAAGAAAC CGGCGGGTTCG  
 \* \*\*\*\*\* \*\* : \* \*\* \*\* \*\*\*\*\* \* \*\* \* \*\*  
 20 : CCGTGCGGA GAT----- ----GAG----- CCAAAGAAGC GTGCTGGACG  
 120 : TAAGAAGTTT CGTGAGACTC GTCACCCAAT ATACAGAGGA GTTCGTCGGA GAAACTCCGG  
 \* \*\* \*\* \*\*\*\*\* \* \*\*\*\*\* \*\*\*\*\* \*\* \*\* \* \*\* \* \*\* \*  
 57 : GAGGATTTTC AAGGAGACAC GTCACCCAAT CTACAGAGGC GTGCGGCGTA GGGACGGCGA  
 180 : TAAGTGGGTT TGTGAGGTTA GAGAACC AAA CAAGAAAACA AGGATTTGGC TCGGAACATT  
 \*\* \*\*\*\*\* \*\* \* \*\* \* \* \*\*\*\*\* \* \* \* \* \* \*\*\*\*\* \*  
 117 : CAAATGGGTA TGCGAAGTCC GTGAACCGAT TCATCAGCGT CGAGTCTGGC TCGGAACTTA  
 240 : TCAAACCGCT GAGATGGCAG CTCGAGCTCA CGACGTTGCC GCTTTAGCCC TTCGTGGCCG  
 \*\* \*\* \*\* \*\* \*\*\*\*\* \* \* \*\* \*\*\*\*\* \*\*\*\*\* \*\* \* \* \* \*\* \* \* \* \*  
 177 : TCCGACGGCA GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TCGCGGGGAG  
 300 : ATCAGCCTGT CTCAATTTCT CTGACTCGGC TTGGAGACTC CGAATCCCGG AATCAACTTG  
 \*\*\* \*\* \*\* \* \*\*\*\*\* \* \*\* \* \*\* \*\*\*\*\* \* \* \* \*\*\*\* \* \*\* \*  
 237 : ATCCGCGTGT TTGAATTTCT CCGATTCTGC TTGGAGGTTG CCGGTGCCG CATCCACT--  
 360 : CGCTAAGGAC ATCCAAAAGG ----CGGCGG CTGAAGCTGC GTTGGCGTTT CAGGATG-AG  
 \* \* \*\*\*\* \* \* \* \*\*\*\* \*\*\*\*\* \* \*\*\*\*\* \*\* \* \* \* \*\* \* \*  
 295 : -GATCCGGAC A-CGATCAGG CGCACGGCGG CCGAAGCAGC GGAGATG-TT CAGGCCGCGG  
 415 : ATGTGTGATG CGACGACGGA TCATGGCTTC GACATGGAGG AGACGTTGGT GGAGGCTATT  
 \*\* \* \* \*\* \* \* \* \* \* \* \* \* \* \* \*\* \* \*\* \* \*\* \*  
 352 : GAGT-TTAGT --AC-AGGAA TTACGGTTTT ACCCT----C AGCC---AGT -GAG---TTT  
 475 : TACACGGCGG AACAGAGCGA AAATGCCGTTT TATATGCACG ATGAGGCGAT GTTTCAGATG

Fig. 2-5

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***** ** * * * * **** * ***** * *** 
397 : GACACGTCGG A--TGA---A GGAGTCGCTG GA-ATG-ATG ATGAGGC--T CGCGGAGGAG

535 : CCCAGTTTG TGT--GCTAAT ATGCCAGA-A GGGATGCTTT TGCCGCTTCC GTCCGTACAG
***      ***   *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *    *
448 : CCGTTGATGT CGCCGCCAAG ATCGTACATT GATATG-AA --ACG----A GTGTGTAC-G

592 : TGGAA TCATA ATCATGAAGT CGACGCGCAT GATGACCAGC TATCGTTATG GAGTTATTAA
****   *  *  *     *          *    *    *    *    *    *    *    *    *    *    *
500 : TGGACGAAGA A--ATG----- -----TGT TACAAGATT TGTCACTTTG GAGTTACTAA

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Sequence 1           : DREB1A.nuc
Size                 : 651
Matching Position    :       1 - 651

Sequence 2           : DREB1F.nuc
Size                 : 630
Matching Position    :       1 - 630

Matching Condition.

Matches              : -1
Mismatches            : 1
Gaps                  : 1
*N+                   : 2

Matching             : 54.81 [%]
Weight               : -21


1 : ATGAACTCAT TTCTGCTTT TTCTGAAAATG TTTGGCTCCG ATTACGAGTC TTCGGTTTTCC
****                **** *        * **                    **
1 : ATGAA----- ---TAATG AT-----G AT----- ----ATTAT

61 : TCAGGCGGTG ATTATATTCC GACGCTTGCG AGCAGCTGCC CCAAGAAACC GGCGGGCTCGT
** ***** * **                      * *         * * ***** * ***** *
21 : TCTGGCGGAG AT----- -----G A-----GGC CTAAGAAGCG TCGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATA TACAGAGGAG TTCGTCGGAG AAACCTCCGT
* ****          ***** ** ***** * ***** * * ***** *** *
58 : AGAGTGTTTA AGGAGACACG TCACCCAGTT TACAGAGGCA TAAGGCGGAG GAACGGTGAC

181 : AAGTGGGTTT GTGAGGTTAG AGAACCAAAC AAAAAACAA GGATTTGGCT CGGAACATTT
** ***** * * ** * ** ***** * * ** * ***** *** ** *
118 : AAATGGGTCT GCGAAGTCAG AGAACCGACG CACCAACGCC GCATTTGGCT CGGCACTAT

241 : CA AACCGCTG AGATGGCAGC TCGAGCTCAC GACGTTGCCG CTITAGCCCT TCGTGCCGA
* ** * * * * ***** ** ** ***** ** * ***** ** ***** **
178 : CCCACAGCAG ATATGGCAGC GCGTGCACAC GACGTGGCGG TTTTAGCTCT GCGTGGGAGA

301 : TCAGCCTGTC TCAATTTGCG TGA CTCGGCT TGGAGACTCC GAATCCCGBA ATCAACTTGC
** ** *** * ***** ***** *** ** * * ** * ***** *** *
238 : TCCGCATGTT TGAATTTGCG C GACTCCGCT TGGCGGCTTC CGGTGCCGA ATCCAATGAT

361 : GCTAAGGACA TCCAAAAGGC GGCGGCTGAA GCTGCGTTGG CGTTTCAGGA TG--AGATGT
* * * * * ** * ***** ** ***** * ***** ** * *** *
298 : CCGGATGTGA TAAGAAGAGT TGCGGCGGAA GCTGCGGAGA TGTT-AGGC CGGTGGATT

419 : -GTGA-TGCG ACGACGGATC ATGGCT--- --CGACATGG AGGAGACGTT GGTGGAGGCT
* * ** * **** * ** ****          **** * * * * *** ** *
357 : AGAAAGTGGA ATTACGG-TT TTGCTTGTG CGGGAGATGA TGTGGATTG GGTTTGGTT
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Fig. 2-6

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472 : ATTTACACGG C----- GGAACAGA-G CGA-AAATGC GT-TTTATAT GCACGATGAG
      *** *          *** * * * * * * * * * * * * * * * *
416 : CGGGTTCCGG CTCTGGTTCG GGATCGGAGG AGAGGAATTC TTCTTCGTAT GGATTGGAG

520 : GCGATGTTTG AGATGCCGAG TTTGTTGGCT AATATGGCAG AAGGGATGCT TTTGCCGCTT
      * * * * * * * * * * * * * * * * * * * * * *
476 : ACTACG-AAG AAGTCTCAAC GACGATGATG AGACTCGCGG AGGGGCCACT AATGTCGCCG

580 : C--CGTCCGT ACAGTGGAA- -----TCA TAATCATG-- -AAGTCGACG --GCGATG--
      * * * * * * * * * * * * * * * * * * * * * *
535 : CCGCGATCGT ATA-TGGAAG ACATGACTCC TACTAATGTT TACACGGAAG AAGAGATGTG

623 : --ATGACGAC GTATCGTTAT GGAGT----- -TATTAA
      **** * * * * * * * * * * * * * * * *
594 : TTATGAAGAT ATGTCATTGT GGAGTTACAG ATATTAA

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Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642

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Sequence 2      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
*N+          : 2

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Matching      : 86.33 [%]
Weight       : -471

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1 : ATGAACTCAT TTTAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TC-----
    ***** * * * * * * * * * * * * * * * * * *
1 : ATGAACTCAT TTTCTGCCTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC

53 : -AAGGCGGAG ATTATTGTCC GACGTTGGCC ACGAGTTGTC CGAAGAAACC GCGGGGCCGT
     ***** * * * * * * * * * * * * * * * * *
61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAG

112 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAATCCGGT
      ***** * * * * * * * * * * * * * * * * *
121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAATCCGGT

172 : AAGTGGGTTT CTGAAGTGAG AGAGCCAAAC AAGAAAACCA GGATTGGCT CGGGACTTTC
      ***** * * * * * * * * * * * * * * * * *
181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGGCT CGGGACTTTC

232 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTCGCTG CATTAGCCCT CCGTGGCCGA
      ***** * * * * * * * * * * * * * * * * *
241 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTCGCGG CCATAGCTCT CCGTGGCAGA

292 : TCAGCATGTC TCAACTTCGC TGAATCGGCT TGGCGGCTAC GAATCCCGGA GTCAACATGC
      ** * * * * * * * * * * * * * * * * * *
301 : TCTGCCTGTC TCAATTTGCG TGAATCGGCT TGGCGGCTAC GAATCCCGGA ATCAACCTGT

352 : GCCAAGGATA TCCAAAAGC GGCTGCTGAA GCGGCGTTGG CTTTTCAAGA TGAGACGTGT
      ***** * * * * * * * * * * * * * * * *

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Fig. 2-7

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361 : GCCAAGGAAA TCCAAAAGGC GCGGCTGAA GCGCGTTGA ATTTTCAAGA TGAGATGTGT
412 : GATACGACGA CCACGAATCA TGGCCTGGAC ATGGAGGAGA CGATGGTGA AGCTATTTAT
    *** ***** *
421 : CATATGACGA CGGATGCTCA TGGTCTTGAC ATGGAGGAGA CCTTGGTGA GGCTATTTAT

472 : ACACCGGAAC AGAGCGAAGG TGCCTTTTAT ATGGATGAGG AGACAATGTT TGGGATGCCG
    ** ***** ***** * ** * ***** ***** *
481 : ACGCCGAAC AGAGCCAAGA TGCCTTTTAT ATGGATGAAG AGGCGATGT GGGGATGTCT

532 : ACTTTGTTGG ATAATATGGC TGAAGGCATG CTTTACC GCCTGTCTGT TCAATGGAAT
    * ***** **** ***** ***** ***** ** *****
541 : AGTTTGTGG ATAACATGGC CGAAGGGATG CTTTACCGT GCCTGTGGT TCAATGGAAC

592 : CATAATTATG ACGCGAAGG AGATGGTGAC GTGTCGCTTT GGAGTTACTA A
    ***** ** * * * * ***** ***** * * ***** ** *
601 : TATAATTTG ATGTCGAGG AGATGATGAC GTGTCCTTAT GGAGCTATTA A

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Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642

Sequence 2      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675

Matching Condition.

Matches          : -1
Mismatched       : 1
Gaps             : 1
*NT              : 2

Matching         : 68.88 [%]
Weight           : -234

1 : ATGAACTCAT TT---TCAGC TTTTCTGAA ATGTTT---- --GGCTCCGA TTA-CGAGC-
    ***** ** * * * * * * * * ***** ***** * * * *
1 : ATGAATCCAT TTTACTCTAC ATTCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT

50 : -----CTC AAGGCGGAGA TTATTGTCCG ACGTTGGCCA CGAGTTGTCC GAAGAAACCG
    * * * * * * * * * * * * * * * * * * * * * * * *
61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA

103 : GCGGGCCGTA AGAAGTTTCG TGAGACTCGT CACCCAATTT ACAGAGGAGT TCGTCAAAGA
    ** ** * * ***** ***** ** ** * * ***** ***** **
121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG

163 : AACTCCGGTA AGTGGGTTTC TGAAGTGAGA GAGCCAAACA AGAAAACCAG GATTTGGCTC
    ** ** **** * ***** ***** ** * ***** * ** ***** *
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTTGGTTA

223 : GGGACTTTCC AAACCGCTGA GATGGCAGCT CGTGCTCAGC ACGTCGCTGC ATTAGCCCTC
    ** ***** * ** * * * ***** ***** * * * * ***** ***** **
241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

283 : CGTGGCCGAT CAGCATGTCT CAATTCGCT GACTCGGCTT GCGGGCTACG AATCCCGGAG
    ***** ** * * * * ***** ** ** ***** ***** ** ** * *
301 : CGTGGTCGCT CTGCTTGCT CAATTCGCT GATTCTGCTT GCGGGCTTCG TATTCCTGAG

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Fig. 2-8

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343 : TCAACATGCG CCAAGGATAT CCAAAAAGCG GCTGCTGAAG CGGCGTTGGC TTTTCAAGAT
      * * * * *
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT

403 : GAGAC----- --GTGTGA-- TACGACGACC AC-GAATCA- TGGCCTGGAC A-TGGAGGAG
      *****
421 : GAGACTACGA CGGAGGGATC TAAAACTGCG GCGGAGGCAG AGGAGGCGGC AGGGGAGGGG

451 : ACGATGGTGG AAGCTATTTA TACACCGGAA CAGAGCGAAG GTGCGTTTTA TATGGATGAG
      ** * * *
481 : GTGAGGGAGG GGGAGAGGAG GCGGAGGAG CAGAATGGTG GTGTGTTTTA TATGGATGAT

511 : GAGACAATGT TTGGGATGCC GACTTTGTG GATAATATGG CTGAAGGCAT GCTTTTACCG
      *** * * *
541 : GAGGCGCTTT TGGGGATGCC CAACTTTTTT GAGAATATGG CGGAGGGGAT GCTTTTGCCG

571 : CCGCCGTCGT TTCAATGGAA TCATAATTAT GACGGCGAAG GAGATGGTGA CGTGTGCTT
      *****
601 : CCGCCGGAAG TTGGTGGAA TCATA---AC GACTTTGACG GAGTGGGTGA CGTGTCACTC

631 : TGGAGTT--- ---ACTAA
      *****
658 : TGGAGTTTTG ACGAGTAA
  
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Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642
  
```

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Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546
  
```

Matching Condition.

```

Matches          : -1
Mismatch         : 1
Gaps              : 1
*N+              : 2

Matching         : 53.38 [%]
Weight          : 2
  
```

```

1 : ATGAACTCAT TTTAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TCAAGGCGGA
   ***
1 : ATG----- -GAAA-- -ACGACG AT----ATCA CCGTGGCGGA

61 : GATTATTGTC CGACGTTGGC CACGAGTTGT CCGAAGAAAC CGGCGGGCCG TAAGAAGTTT
   ***
30 : GAT----- -GA----- -AG----- CCAAGAAGC GTGCTGGACG GAGGATTTTC

121 : CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAAA GAAACTCCGG TAAGTGGGTT
     *****
67 : AAGGAGACAC GTCACCCAAT CTACAGAGGC GTGCGGCGTA GGGACGGCGA CAAATGGGTA

181 : TCTGAAGTGA GAGAGCCAAA CAAGAAAACC AGGATTGGC TCGGGACTTT CCAAACCGCT
   * * * * *
127 : TGCGAAGTCC GTGAACCGAT TCATCAGCGT CGAGTCTGGC TCGGAACCTA TCCGACGGCA

241 : GAGATGGCAG CTCGTGCTCA CGACGTCGCT GCATTAGCCC TCCGTGGCCG ATCAGCATGT
   ** * * *
187 : GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TGCGCGGGAG ATCCGCGTGT
  
```

Fig. 2-9

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```

301 : CTCAACTTCG CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAAC--A TCGCCCAAGG
    * ** * * * * * * * * * * * * * * * * * * * * * * * * * *
247 : TTGAATTCT CCGATTCTGC TTGGAGGTTG CCGGTGCCGG CATCCACTGA TCCGGACACG

359 : AT-ATCCAAA AAGCGGCTGC TGAAGCGGCG TTGGCTTTTC AAGATG-AGA CGTGTGATAC
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
307 : ATCAGGCGCA ---CGGCGGC CGAAGCAGCG -GAGATGTT AGGCCGCCGG AGTTTAGTAC

417 : GACGACCACG AATCATGGCC T-GGACATGG AG---GAGAC GATGGTGGAA GCTATTATA
    * * * * * * * * * * * * * * * * * * * * * * * * * *
363 : AGGAATTACG -GTTTACCC TCAGCCAGTG AGTTTGACAC GTCGGATGAA G-----GAGT

473 : CACCGGAACA GAGCGAAGGT GCGTTTTATA TGGATGAGGA GACAATGTTT GGGATGCCGA
    * * * * * * * * * * * * * * * * * * * * * * * * * *
417 : CGCTGGAA-- ---TGATGAT GAG-----GC TCGCGGAGGA GCCGTTGATG TCGCCGCCAA

533 : CTTTGTGGGA TAATATGGCT GAAGGCATGC TTTTACCGCC GCCGTCTGTT CAATGGAATC
    * * * * * * * * * * * * * * * * * * * * * * * * * *
467 : GATCGTACAT TGATA----T GAA----- ---TAC---- -GAGTGTGA C-GTGGACGA

593 : ATAATTATGA CGGCGAAGGA GATGGTGACG TGTCGCTTTG GAGTTACTAA
    * * * * * * * * * * * * * * * * * * * * * * * * * *
507 : AGAAATGTG- TTACGAA--- -----GATT TGTCACTTTG GAGTTACTAA

```

+++++

```

Sequence 1      : DREB1B.nuc
Size            : 642
Matching Position : 1 - 642

Sequence 2      : DREB1F.nuc
Size            : 630
Matching Position : 1 - 630

```

## Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
* N +            : 2

Matching          : 56.23 [%]
Weight            : -34

```

```

1 : ATGAACTCAT TTTCAGCTTT TTCTGAAATG TTTGGCTCCG ATTACGAGCC TCAAGGCGGA
    ***** * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGAA-TAAT GATGATATTA TTCT----- -----GCGGGA

61 : GATTATTGTC CGACGTTGGC CACGAGTTGT CCGAAGAAAC CGGCGGGCCG TAAGAAGTTT
    *** * * * * * * * * * * * * * * * * * * * * * * *
30 : GAT----- ---GA---GG CCTAAGAAGC GTGCGGGAAG GAGAGTGTTC

121 : CGTGAGACTC GTCACCCAAT TTACAGAGGA GTTCGTCAAA GAAACTCCGG TAAGTGGGTT
    ***** * * * * * * * * * * * * * * * * * * * * *
67 : AAGGAGACAC GTCACCCAGT TTACAGAGGC ATAAGGCGGA GGAACGGTGA CAAATGGGTC

181 : TCTGAAGTGA GAGAGCCAAA CAAGAAAACC AGGATTGTC TCGGGACTTT CCAAACCGCT
    * * * * * * * * * * * * * * * * * * * * * * * * * *
127 : TGCGAAGTCA GAGAACCGAC GCACCAACGC CGCATTGTC TCGGGACTTA TCCCACAGCA

241 : GAGATGGCAG CTCGTGCTCA CGACGTCGCT GCATTAGCCC TCGTGGCCG ATCAGCATGT

```

Fig. 2-10

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```

187 : ** ***** * ***** ** ***** ** * ***** * * ***** * *** *****
      GATATGGCAG CGCGTGCACA CGACGTGGCG GTTTTAGCTC TCGTGGGAG ATCCGCATGT

301 : CTCAACTTCG CTGACTCGGC TTGGCGGCTA CGAATCCCGG AGTCAACATG CGCC-AAGGA
      * ** **** * ***** ** ***** * * **** * * * *** ** * *

247 : TTGAATTCG CCGACTCCGC TTGGCGGCTT CCGGTGCCG AATCCA-ATG ATCCGGATGT

360 : TATCCAAAAA GCGGCTGCTG AAGCGGCGTT GGCTTTTCAA GATGAGACGT GTGATACGAC
      ** * * * * * * * * * * * * * * * * * * * * * * * *

306 : GATAAGAAGA GTTGGCGCGG AAGCTGCGGA GATGTTTAGG CCGGTGGATT TAGAAAGTGG

420 : GACCACGAAT ----CATGGC CTGGACATG- -GAGGA---- GACGATGGT- --GG---AAG
      * *** * * * * * * * * * * * * * * * * * * * * * *

366 : AATTACGGTT TTGCCTTG TGCGGAGATGA TGTGGATTTG GGTTTTGGTT CGGGTTCCGG

464 : CTAT--TTAT ACACCGGAAC AGAGCGAAGG TCGGT-TTTA TATGGATGAG GAGACAATGT
      ** * ** * * **** * * * * * * * * * * * * * * * * * *

426 : CTCTGGTTTG GGATCGGAGG AGAG-GAA-- TTCTTCTTG TATGGATTTG GAGACTACG-

521 : TTGGGATGCC GACTTTGTTG GATAATA-TG GCTGAAGG-- CA-TGCTTTT ACCGCCGC--
      * * * * * * * * * * * * * * * * * * * * * * *

482 : AAGAAGTCTC AACGACGAT- GATGAGACTC GCGGAGGGGC CACTAATGTC GCCGCCGCGA

575 : -CGTCTGTTT AA---TGGAA TCATAATTAT G-----ACGG CGAAGGAGAT G-GT-----
      *** * * * * * * * * * * * * * * * * * * * * * *

541 : TCGTATATGG AAGACATGAC TCCTACTAAT GTTTACACGG AAGAAGAGAT GTGTTATGAA

619 : GACGTGTCGC TTTGGAGTTA C-----TAA
      ** **** * ***** * * *

601 : GATATGTCAT TGTGGAGTTA CAGATATTAA
  
```

+++++

```

Sequence 1      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651
  
```

```

Sequence 2      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675
  
```

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
#N+          : 2

Matching      : 68.34 [%]
Weight       : -233
  
```

```

1 : ATGAACTCAT TT---TCTGC CTTTCTGAA ATGTTT---- --GGCTCCGA TTACGAGTCT
      ***** ** * * * * * * * * * * * * * * * * * *

1 : ATGAATCCAT TTTACTCTAC ATTCCAGAG TCGTTTCTCT CAATCTCCGA TCATAGATCT

52 : CCGGTTTCCT CAGGCGGTGA TTACAGTCCG AAGCTTGCCA CGAGCTGCC CAAGAAACCA
      ***** * **** * ** *** * * * * * * * * * *

61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACCA

112 : GCGGGAAGGA AGAAGTTTCG TGAGACTCGT CACCCAATTT ACAGAGGAGT TCGTCAAAGA
      ** ** **** ***** * * * * * * * * * * * * * *

121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG
  
```

Fig. 2-11

0009114

```

172 : AACTCCGGTA AGTGGGTGTG TGAGTTGAGA GAGCCAAACA AGAAAACGAG GATTGGCTC
    ** ** ** * ** ** * ** * ** * ** * ** * ** * ** * ** *
181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTGGTTA

232 : GGGACTTTCC AAACCGCTGA GATGGCAGCT CGTGCTCAGC ACGTCGCCGC CATAGCTCTC
    ** ** ** * ** * ** * ** * ** * ** * ** * ** * ** *
241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT

292 : CGTGGCAGAT CTGCCTGTCT CAATTTGCT GACTCGGCTT GCGGGCTACG AATCCCGGAA
    ***** * ** * ** * ** * ** * ** * ** * ** * ** *
301 : CGTGGTGCCT CTGCTTGTCT CAATTTGCT GATTCTGCTT GCGGGCTTCG TATTCTGAG

352 : TCAACCTGTG CCAAGGAAAT CCAAAAGGCG GCGGCTGAAG CCGCGTTGAA TTTTCAAGAT
    * ** * ** * ** * ** * ** * ** * ** * ** * ** *
361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT

412 : GAGA----- -TGTGTCATA TGA-----CG ACGGATGCTC ATGGTCTTGA CA-TGGAGGA
    **** : * * ** * * ** **** ** * ** * ** *
421 : GAGACTACGA CGGAGGGATC TAAAACTGCG GCGGAGGCAG A-GGAGGCGG CAGGGGAGGG

459 : GACCTTGGTG GAGGCTATTT ATACGCCGGA ACAGAGCCAA GATGCGTTTT ATATGGATGA
    * ** * ** * ** * ** * ** * ** * ** * ** *
480 : GGTGAGGGAG GGGAGAGGA GGGCGGAGGA GCAGAATGGT GGTGTGTTTT ATATGGATGA

519 : AGAGGCGATG TTGGGGATGT CTAGTTTGTG GGATAACATG GCCGAAGGGA TGCTTTTACC
    ***** * ** * ** * ** * ** * ** * ** * ** *
540 : TGAGGCGCTT TTGGGGATGC CCAACTTTTT TGAGAATATG GCGGAGGGGA TGCTTTTGCC

579 : GTCCCGCTCG GTTCAATGGA ACTATAATTT TGATGTCGAG GGAGATGATG ACGTGTCTT
    * ***** ** * ** * ** * ** * ** * ** *
600 : GCCGCCGGAA GTTGGCTGGA ATCATAA--- CGACTTTGAC GGAGTGGGTG ACGTGTCACT

639 : ATGGAG---- --CTATTAA
    ***** * * **
657 : CTGGAGTTTT GACGAGTAA

```

+++++

```

Sequence 1      : DREB1C.nuc
Size            : 651
Matching Position : 1 - 651

```

```

Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 54.95 [%]
Weight       : 1

```

```

1 : ATGAACTCAT TTTCTGCCTT TTCTGAAATG TTTGGCTCCG ATTACGAGTC TCCGGTTTCC
    ***                **** * ** * ** *
1 : ATG----- -----GAAA-- ----ACGACG AT-----ATC ACCG-----

61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG
    ***** * **                * * ***** * ** * **

```

Fig. 2-12

0009114

```

23 : --TGGCGGAG AT----- GAAG----- -----C CAAAGAAGCG TGCTGGACGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAACCTCCGGT
    * ** **      ***** ** ***** ***** * * * * ** ** **
58 : AGGATTTTCA AGGAGACACG TCACCCAATC TACAGAGGCG TCGGGCGTAG GGACGGCGAC

181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGA-TTTGGC TCGGGACTTT
    ** ***** * * * * * ** * * * * * * * * * * * * * * *
118 : AAATGGGTAT GCGAAGTCCG TGAACCGATT CA-TCAGCGT CGAGTCTGGC TCGGAACCTA

240 : CCAAACCGCT GAGATGGCAG CTCGTGCTCA CGACGTGCGC GCCATAGCTC TCCGTGGCAG
    * ** ** * * ***** * * ***** ***** * * * * * * * *
177 : TCCGACGGCA GATATGGCCG CACGTGCTCA CGACGTGGCG GTTCTTGCTC TCGCGGGGAG

300 : ATCTGCCTGT CTCAATTTTC CTGACTCGGC TTGGCGGCTA CGAATCCCGG AATCAACCTG
    *** ** ** * * ***** * * * * * ***** * * * * * * * *
237 : ATCCGCGTGT TTGAATTTCT CCGATTCTGC TTGGAGGTTG CCGGTGCCGG CATCCA-CTG

360 : TGCCAAGGAA ATCCAAAAGG ----CGGCGG CTGAAGCCGC GTTGAATTTT CAAGATGAGA
    ** *** * * * * * ***** * ***** * * * * * * * *
296 : ATCC--GGAC A-CGATCAGG CGCACGGCGG CCGAAGCAGC GGAG-ATGTT CAGGCCG-CC

416 : TGTGTCATAT GACGACGGAT GCTCATGGTC TTGACATGGA GGAGACCTTG GTGGAGGCTA
    * ** ** * * ***** * * * * * ** * * * * * * * *
351 : GGAGT-TTAG TAC--AGGA- -ATTACGGTT TTACCCT--- -CAG-CC--A GT-GAG---T

476 : TTTATACGCC GGAACAGAGC CAAGATGCGT TTTATATGGA TGAAGAGCGG ATGTTGGGGA
    ** * *** * *** ** * * * * * * * * * * * * * * * * * *
395 : TTGACACGTC GGA--TGA-- -AGGAGTCGC TGGA-AT-GA TGATGAGGC- ---TCGCGGA

536 : TGTCTAGTTT GT-TGGATAA CATGGCCGAA GGGATGCTTT TACCGTCGCC GTCGGTTCAA
    * *** * * * * * * * * * * * * * * * * * * * *
444 : GGAGCCGTTG ATGTCGCCGC CAAGATCGTA -CATTGATAT GA--ATACGA GTGTGTAC-G

595 : TGGAACATA ATTTTGATGT CGAGGGAGAT GATGACGTGT CCTTATGGAG CTATTAA
    ***** * * * * * * * * * * * * * * * * * * * *
500 : TGGACGAAGA A-----ATGT -----GTTAC GAAGATTTGT CACTTTGGAG TTAATAA
  
```

+++++

```

Sequence 1      : DREB1C.nuc
Size           : 651
Matching Position : 1 - 651
  
```

```

Sequence 2      : DREB1F.nuc
Size           : 630
Matching Position : 1 - 630
  
```

Matching Condition.

```

Matches       : -1
Mismatches    : 1
Gaps          : 1
* N+          : 2

Matching      : 56.10 [%]
Weight       : -35
  
```

```

1 : ATGAACATCAT TTTCTGCCTT TTCTGAAATG TTGGCTCCG ATTACGAGTC TCCGGTTTCC
    *****      * * * * *
1 : ATGAA-----TAATG AT-----G AT-----ATTAT
  
```

Fig. 2-13

0009114

```

61 : TCAGGCGGTG ATTACAGTCC GAAGCTTGCC ACGAGCTGCC CCAAGAAACC AGCGGGAAGG
    ** ***** **
21 : TCTGGCGGAG AT----- --GA---GGC CTAAGAAGCG TCGGGAAGG

121 : AAGAAGTTTC GTGAGACTCG TCACCCAATT TACAGAGGAG TTCGTCAAAG AAACCTCCGGT
    * **** ***** ** ***** * * * ** *
58 : AGAGTGTTTA AGGAGACACG TCACCCAGTT TACAGAGGCA TAAGGCGGAG GAACGGTGAC

181 : AAGTGGGTGT GTGAGTTGAG AGAGCCAAAC AAGAAAACGA GGATTGGCT CGGGACTTTC
    ** ***** * * * * * * * * * * * * * * *
118 : AAATGGGTCT GCGAAGTCAG AGAACCAGCG CACCAACGCC GCATTGGCT CGGGACTTAT

241 : CAAACCGCTG AGATGGCAGC TCGTGCTCAC GACGTGCGCG CCATAGCTCT CCGTGGCAGA
    * * * * * * * * * * * * * * * * * * *
178 : CCCACAGCAG ATATGGCAGC GCGTGCACAC GACGTGGCGG TTTAGCTCT GCGTGGGAGA

301 : TCTGCCTGTC TCAATTTGCG TGA CTGCGCT TGGCGGCTAC GAATCCCGGA ATCAACCTGT
    ** * * * * * * * * * * * * * * * * * *
238 : TCCGCATGTT TGAATTTGCG CGACTCCGCT TGGCGGCTTC CGGTGCCGGA ATCCAATGAT

361 : GCCAAGGAAA TCCAAAAGGC GCGCGGTGAA GCCGCGTTGA ATTTTCAAGA TG--AGATGT
    * * * * * * * * * * * * * * * * * * *
298 : CCGGATGTGA TAAGAAGAGT TCGGCGGAA GCTGCGGAG- ATGTTTAGGC CGGTGGATT

419 : GTCATATG-- ACGACGGATG CTCATGGT-C TTGACATG-- GAGGA----G ACCTTGGTGG
    * * * * * * * * * * * * * * * * *
357 : AGAAAGTGA ATTACGGTTT TGCCTTGTC GGGAGATGAT GTGGATTGG GTTTTGGTTC

470 : AGGCTATTTA TACG---CCG GAACAGAGCC AAG--ATGCG T-TTTATATG GATGAAGAGG
    * * * * * * * * * * * * * * * * *
417 : GGGTTCGGC TCTGGTTCGG GATCGGAGGA GAGGAATTCT TCTTCGTATG GATTGGAGA

524 : CGATGTTGGG GATGTCTAGT TTGTTGGATA ACA-TGGCCG AAGGGATGCT TTTACCGTCG
    * * * * * * * * * * * * * * * * *
477 : CTACGAAGAA G-TCTCAACG ACGAT-GATG AGACTCGCGG AGGGGCCACT AATGTCGCCG

583 : CCGTCCGT-- TCAATGGAA- -----C TA-TAATTTT GATGTCGAGG --GAGATG--
    *** * * * * * * * * * * * * * * *
535 : CCG-CGATCG TATATGGAAG ACATGACTCC TACTAATGTT TACACGGAAG AAGAGATGTG

626 : --ATGACG-- -TGTCCTTAT GG-----AG CTATTAA
    **** * **** * * * * *
594 : TTATGAAGAT ATGTCATTGT GGAGTTACAG ATATTAA
  
```

+++++

```

Sequence 1      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675
  
```

```

Sequence 2      : DREB1E.nuc
Size            : 546
Matching Position : 1 - 546
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 51.26 [%]
Weight            : 29
  
```

Fig. 2-14

0009114

```

1 : ATGAATCCAT TTTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT
   ***                               **          ** * *** *      ***
1 : ATG-----GA-----AAACGACGA T-----ATCA

61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA
   ** ** * * *      **          * *** ** ***** **
20 : CC-GTGGCGG A-----GA-----T GAAG----CC AAAGAAGCGT

121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG
   ***** ** ** ***** ** ** * * ***** ** ** * ***
49 : GCTGGACGGA GGATTTTCAA GGAGACACGT CACCCAATCT ACAGAGGCGT GCGGCGTAGG

181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAATCTAG GATTGGTTA
   * * * ***** ** ***** * ** * * * * * * * * * *
109 : GACGGCGACA AATGGGTATG CGAAGTCCGT GAACCGATTG ATCAGCGTCG AGTCTGGCTC

241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT
   ** ***** ** ***** ** ***** * * * * * * * * * *
169 : GGAACATTATC CGACGGCAGA TATGGCCGCA CGTGCTCAGC ACGTGGCGGT TCTTGCTCTG

301 : CGTGGTCGCT CTGCTGTCT CAATTTCTGCT GATTCTGCTT GGCGGCTTCG TATTCCTGAG
   ** * * * * * * * * * * ***** * ***** ** * * * * *
229 : CGCGGGAGAT CCGCGTGTG GAATTTCTCC GATTCTGCTT GGAGGTTGCC GGTGCCGGCA

361 : ACTACTTGTC CTAAGGAGAT TCAGAAAGCT GCGTCTGAAG CTGCAATGGC GTTTCAGAAT
   * *** ** * * * * * * * * * * * * * * * * * * * *
289 : TCCACTGATC CGGACACGAT CAGGCGCAGC GCGGCCGAAG CAGCGGAGAT G-TTCAG---

421 : GAGACTACGA CGGAGGGATC TAAACTGCG GCGGAGGCAG AGGAGGCGGC AGGGGAGGGG
   ** ***** * ** * * * * * * * * * * * * * * * *
345 : -----GCCGC CGGAG---TT TAGTACAG-G AATTA--CGG TTTACCCTC A-GCCAGTGA

481 : GTGAGGGAGG GGGAGAGGAG GCGGAGGAG CAGAATGGTG GTGTGTTTTA TATGGATGAT
   ** * * * * * * * * * * * * * * * * * * * * * * *
393 : GTTTGACACG TCG-GATGAA GGAGTCGCTG --GAATGATG ATGAG----- GCTCGCGGAG

541 : GAGGCGCTTT TGGGATGCC CAACTTTTTT GAGAATATGG CCGAGGGGAT GCTTTTGCCG
   *** * * * * * * * * * * * * * * * * * * * * * *
445 : GAGCCGTTGA TGTGCGCGCC AAGATCGTAC ATTGATAT-- ----GAAT ACGAGT---

601 : CCGCCGGAAG TTGGCTGGAA TCATAACGAC TTTGACGGAG TGGGTGACGT GTCACCTG
   * * * * * * * * * * * * * * * * * * * * * * *
494 : ----TGACG TGGAC--GAA --GAAATG-- TGTACGAA-- ----GATT GTCACCTG

661 : AGTTTTGACG AGTAA
   ****          * ***
538 : AGTT----- ACTAA

```

+++++

```

Sequence 1      : DREB1D.nuc
Size            : 675
Matching Position : 1 - 675

```

```

Sequence 2      : DREB1F.nuc
Size            : 630
Matching Position : 1 - 630

```

Matching Condition.

Fig. 2-15

0009114

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
* N+         : 2

```

```

Matching     : 54.92 [%]
Weight       : -24

```

```

1 : ATGAATCCAT TTTACTCTAC ATTCCCAGAC TCGTTTCTCT CAATCTCCGA TCATAGATCT
    *****                               *** ** * *** *
1 : ATGAAT----- -AAT-----GA TGATATTATT

61 : CCGGTTTCAG ACAGTAGTGA GTGTTACCA AAGTTAGCTT CAAGTTGTCC AAAGAAACGA
    * ** * * * * * * * * * * * * * * * * * * * * * *
22 : CTGG---CGG AGA---TGA -----GGCC TAAGAAGCGT

121 : GCTGGGAGGA AGAAGTTTCG TGAGACACGT CATCCGATTT ACAGAGGAGT TCGTCAGAGG
    ** ** * * * * * * * * * * * * * * * * * * * * *
49 : GCGGGAAGGA GAGTGTTTAA GGAGACACGT CACCCAGTTT ACAGAGGCAT AAGGCGGAGG

181 : AATTCTGGTA AATGGGTTTG TGAAGTTAGA GAGCCTAATA AGAAATCTAG GATTTGGTTA
    ** ** * * * * * * * * * * * * * * * * * * * * *
109 : AACGGTGACA AATGGGCTCG CGAAGTCAGA GAACCGACGC ACCAACGCCG CATTGGCTC

241 : GGTACTTTTC CGACGGTTGA AATGGCTGCT CGTGCTCATG ATGTTGCTGC TTTAGCTCTT
    ** ** * * * * * * * * * * * * * * * * * * * * *
169 : GGGACTTATC CCACAGCAGA TATGGCAGCG CGTGACACAG ACGTGGCGGT TTTAGCTCTG

301 : CGTGGTCGCT CTGCTTGCTT CAATTTGCTT GATTCTGCTT GCGGGCTTCG TATTCCTGAG
    ***** * * * * * * * * * * * * * * * * * * * *
229 : CGTGGGAGAT CCGCATGTTT GAATTTGCCC GACTCCGCTT GCGGGCTTCC GGTGCCGGAA

361 : ACTACTTGTC CTAAGGAGAT TCAGAA-AGC TGCCTCTGAA GCTGCAATGG CGTTTCAGAA
    * * * * * * * * * * * * * * * * * * * * * * *
289 : TCCAATGATC CGGATGTGA- TAAGAAGAGT TCGGCGGAA GCTGCGGAGA TGTTTAGGCC

420 : TG-AGACTAC GACGGAGGGA TCTAAACTG CGGC---GGA GGCAGAGGAG GCGG-CAGGG
    * * * * * * * * * * * * * * * * * * * * * * *
348 : GGTGGATTTA GAAAGTGGA T-TACGGTTT TGCCTTGTGC GGGAGATGAT GTGGATTG

475 : GAGGGGGTGA GGG---AGGG GGAGAGGAGG G--CGGAGGA GCAGAATGGT GGTGTGTTTT
    * * * * * * * * * * * * * * * * * * * * * * *
407 : GTTTTGTTTC GGGTCCGGC TCTGTTTCG GATCGGAGGA GAGGAAT--- --TCTCTTC

530 : ATATGGATGA TGAGGCGCTT TTGGGGATG- CCCAACTTTT TTGA-GAATA TGGCGGAGGG
    ***** * * * * * * * * * * * * * * * * * * *
462 : GTATGGATTT GGAGAC---T ACGAAGAAGT CTCAACGACG ATGATGAGAC TCGCGGAGGG

588 : GATGCTTTTG CCGCCGCCG- GAAGTTGGCT GGAA-TCATA A---CGAC-- ----TTTGAC
    * * * * * * * * * * * * * * * * * * * * * * *
519 : GCCACTAATG TCGCCGCCG GATCGTATAT GGAAGACATG ACTCCTACTA ATGTTTACAC

637 : GGA----- --GTG---G GTGACGTGTC ACTCTGGAGT TTTGACGAGT AA
    *** * * * * * * * * * * * * * * * * * * *
579 : GGAAGAAGAG ATGTGTTATG AAGATATGTC ATTGTGGAGT TACAGATATT AA

```

+++++

```

Sequence 1 : DREB1E.nuc
Size       : 546

```



Fig. 2-16

0009114

Matching Position : 1 - 546

Sequence 2 : DREB1F.nuc  
 Size : 630  
 Matching Position : 1 - 630

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 69.26 [%]  
 Weight : -221

```

1 : ATGGAACG ACGATATCAC CGTGGCGGAG ATGAAGCCAA AGAAGCGTGC TGGACGGAGG
   *** * ** * * ***** * ***** **** * * ***** *** ****
1 : ATGAATAATG ATGATATTAT TCTGGCGGAG ATGAGGCCTA AGAAGCGTGC GGAAGGAGA

61 : ATTTTCAAGG AGACACGTCA CCCAATCTAC AGAGGCGTGC GCGGTAGGGA CGGCGACAAA
   * ** ***** ***** * *** ***** * **** * * * * *****
61 : GTGTTTAAGG AGACACGTCA CCCAGTTTAC AGAGGCATAA GCGGAGGAA CGGTGACAAA

121 : TGGGTATGCG AAGTCCGTGA ACCGATTTCAT CAGCGTCGAG TCTGGCTCGG AACTTATCCG
   ***** * * * * * * * * * * * * * * * * * * * * * * * *
121 : TGGGTCTGCG AAGTCAGAGA ACCGACGCAC CAACGCCGCA TTTGGCTCGG GACTTATCCC

181 : ACGGCAGATA TGGCCGCACG TGCTCAGCAC GTGGCGGTTT TTGCTCTGCG CGGGAGATCC
   ** ***** * * * * * * * * * * * * * * * * * * * * * *
181 : ACAGCAGATA TGGCAGCGCG TGCACACGAC GTGGCGGTTT TAGCTCTGCG TGGGAGATCC

241 : GCGTGTTTGA ATTTCTCCGA TTCTGCTTGG AGGTTGCCGG TGCCGGCATC CACTGATCCG
   ** ***** * * * * * * * * * * * * * * * * * * * * * *
241 : GCATGTTTGA ATTTGCGCGA CTCGCTTGG CGGCTTCCGG TGCCGGAATC CAATGATCCG

301 : GACACGATCA GCGGCACGGC GGCCGAAGCA GCGGAGATGT TCAGGCCGCC GGAGTTTAG-
   ** * * * * * * * * * * * * * * * * * * * * * * * *
301 : GATGTGATAA GAAGAGTTGC GCGGAAGCT GCGGAGATGT TTAGGCCGGT GGA-TTTAGA

360 : TACAGGAATT ACGGTTTTAC CCTCAGC--C AG----- ----TGAGTT T-----
   * ***** * * * * * * * * * * * * * * * * * * * * *
360 : AAGTGAATT ACGGTTTTGC CTTGTGCGGG AGATGATGTG GATTTGGGT TTGGTTCCGG

397 : ----- ----GACA- ----- -CGT-CGGAT -----
   * * * * * * * * * * * * * * * * * * * * *
420 : TTCCGGCTCT GGTTCGGGAT CGGAGGAGAG GAATTCTTCT TCGTATGGAT TTGGAGACTA

409 : -GAAGGAGTC GCTGGAATGA TGATGAGGCT CGCGGAGGAG CCGTTGATGT CGCCGCCAAG
   ***** * * * * * * * * * * * * * * * * * * * * *
480 : CGAAGAAGTC TCAACGACGA TGATGAGACT CGCGGAGGGG CCACTAATGT CGCCGCCGCG

468 : ATCGTACAT- --TGATATGA ---ATACGAG TGTGTACGTG GACGAAGAAA TGTGTTACGA
   ***** * * * * * * * * * * * * * * * * * * * * *
540 : ATCGTATATG GAAGACATGA CTCCTACTAA TGTTTACAGG GAAGAAGAGA TGTGTTATGA

522 : AGATTTGTCA CTITGGAGTT AC-----TA A
   ***** * * * * * * * * * * * * * * *
600 : AGATATGTCA TTGTGGAGTT ACAGATATTA A
  
```

Fig. 3-1

0046368

[GENETYX-MAC: Maximum Matching]  
Date : 2003.03.03

+++++

Sequence 1 : DREB1A.aa  
Size : 216  
Matching Position : 1 - 216

Sequence 2 : DREB1B.aa  
Size : 214  
Matching Position : 1 - 214

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 85.78 [%]  
Weight : -148

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
*****
1 : MNSFSAFSEM FGSDYE---P QGGDYCPTLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

61 : K WVCEVREPN KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLN FADSA WRLRIPESTC
***
58 : K WVSEVREPN KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLN FADSA WRLRIPESTC

121 : AKDIQKAAAE AALAFQDEMC D-ATTDHGFD MEETLVEAIY TAEQSENAFY MHDEAMFEMP
*****
118 : AKDIQKAAAE AALAFQDETC DTTTTHGLD MEETMVEAIY TPEQSEGA FY MDEETMFGMP

180 : SLLANMAEGM LLPLPSVQWN HNHEVDGDDD DVSLWSY-
**
178 : TLLDNMAEGM LLPPPSVQWN HNYDGEG-DG DVSLWSY*
```

+++++

Sequence 1 : DREB1A.aa  
Size : 216  
Matching Position : 1 - 216

Sequence 2 : DREB1C.aa  
Size : 217  
Matching Position : 1 - 217

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 86.70 [%]  
Weight : -154

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
*****
1 : MNSFSAFSEM FGSDYESPV SGGDYSPKLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

61 : K WVCEVREPN KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLN FADSA WRLRIPESTC
*****
```

Fig. 3-2

0046368

```

61 : KVVCELREP KTRIWLGT QTAEMAARAH DVAALRGR SACLNFADSA WRLRIPESTC

121 : AKDIQKAAAE AALAFQDEMC DATTD-HGFD MEETLVEAIY TAEQSENAFY MHDEAMFEMP
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
121 : AKEIQKAAAE AALNFQDEMC HMTTDAHGLD MEETLVEAIY TPEQSQDAFY MDEEAMLGMS

180 : SLLANMAEGM LLPLPSVQWN HNHEVDGDDD DVSLWSY-
    *** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
181 : SLLDNMAEGM LLPSPSVQWN YNFDVEG-DD DVSLWSY*
  
```

+++++

```

Sequence 1      : DREB1A.aa
Size            : 216
Matching Position : 1 - 216
  
```

```

Sequence 2      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224
  
```

Matching Condition.

```

Matches          : -1
Mismatch         : 1
Gaps             : 1
*N+              : 2

Matching         : 65.04 [%]
Weight           : -56
  
```

```

1 : MNSF-SAF-- SEMFGSDYES SVSSGGDYIP TCLASSCPKKP AGRKKFRETR HPIYRGVRRR
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSK KCLASSCPKKR AGRKKFRETR HPIYRGVRQR

58 : NSGKWVCEVR EPNKKTRIWL GTFQTAEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    ***** * * * * * * * * * * * * * * * * * * * * * * * *
61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE

118 : STCAKDIQKA AEAALAFQD EMCDATTDHG FDMEETLVE- ----AIYTAE QSENAFYMH
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * *
121 : TTCPEIQKA ASEAAAFQN ETTTEGSKTA AEAEAAEGEG VREGERRAE QNGGVFYMD

173 : EAMFEMPSLL ANMAEGMLLP LPSVQWNHNNH EVDGDDDDVS LWS--Y
    ** * * * * * * * * * * * * * * * * * * * * * * * * * * *
181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHN- DFDG-VGDVS LWSFDE
  
```

+++++

```

Sequence 1      : DREB1A.aa
Size            : 216
Matching Position : 1 - 216
  
```

```

Sequence 2      : DREB1E.aa
Size            : 181
Matching Position : 1 - 181
  
```

Matching Condition.

```

Matches          : -1
Mismatch         : 1
Gaps             : 1
*N+              : 2

Matching         : 45.87 [%]
Weight           : 32
  
```

Fig. 3-3

0046368

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
  * * * * *
1 : M----- -ENDDI-TVA EMKPKKRAGR RIFKETRHP I YRGVRRRDGD

61 : K WVCEVREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLN FADSA WRLRIPESTC
  * * * * *
40 : K WVCEVREP I HQRRVWLGT Y PTADMAARAH DVAVLALRGR SACLN FSDSA WRLPVPASTD

121 : AKDIQKAAAE AALAFQDEMC DATTDHGFD M EETLVEAIYT AEQSENAFY M HDEAMFEMPS
  * * * * *
100 : PDIIRRTAAE AA-----EM- -----FRP PE--FSTGIT VLPSASEFDT SDEGVAGMMM

181 : LLANMAEGML LPLPSVQWNH NHEVD--GDD DDVSLWSY
  * * * * *
145 : RLA-EEPLMS PPRS YIDMNT SVYVDEEMCY EDLSLWSY
  
```

+++++

```

Sequence 1      : DREB1A.aa
Size            : 216
Matching Position : 1 - 216

Sequence 2      : DREB1F.aa
Size            : 209
Matching Position : 1 - 209
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 43.91 [%]
Weight       : 42
  
```

```

1 : MNSFSAFSEM FGSDYESSVS SGGDYIPTLA SSCPKKPAGR KKFRETRHPI YRGVRRRNSG
  * * * * *
1 : MN----- -NDDI-ILA EMRPKKRAGR RVFKETRHPV YRGIRRRNGD

61 : K WVCEVREP N KKTRIWLGT F QTAEMAARAH DVAALALRGR SACLN FADSA WRLRIPESTC
  * * * * *
40 : K WVCEVREP T HQRRVWLGT Y PTADMAARAH DVAVLALRGR SACLN FADSA WRLPVPESND

121 : AKDIQKAAAE AALAF--QDE MCDAT--TDH GFDMEETLVE AIYTAEQSE- -NAFYMHDEA
  * * * * *
100 : PDVIRRVAAE AAEMFRPVDL ESGITVLPCA GDDVDLGFSG GSGSGSGSEE RNSSSYGFGD

175 : MFEMPSLLAN MAEGMLLPLP -----SVQW NNNHEVDGDD DDVSLWS--Y
  * * * * *
160 : YEEVSTTMMR LAEGPLMSPP RSYMEDMTPT NVYTEEMCY EDMSLWSYRY
  
```

+++++

```

Sequence 1      : DREB1B.aa
Size            : 213
Matching Position : 1 - 213

Sequence 2      : DREB1C.aa
Size            : 217
Matching Position : 1 - 217
  
```

Fig. 3-4

0046368

## Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
* N+         : 2

Matching      : 86.18 [%]
Weight       : -153

```

```

1 : MNSFSAFSEM FGSDYE---P QGGDYCPTLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG
   *****
1 : MNSFSAFSEM FGSDYESPVS SGGDYSPKLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG

58 : K WVSEVREPN KKTRIWLGT FQTAEMAARAH DVAALALRGR SACLNFA DSA WRLRIPESTC
    *** * ****
61 : K WVCELREPN KKTRIWLGT FQTAEMAARAH DVAALALRGR SACLNFA DSA WRLRIPESTC

118 : AKDIQKAAAE AALAFQDETC DTTTTNHGLD MEETMVEAIY TPEQSEGAFY MDEETMFGMP
    ** ***** ** * ****
121 : AKEIQKAAAE AALNFQDEMC HMTTDAHGLD MEETLVEAIY TPEQSQDAFY MDEEAMLGMS

178 : TLLDNMAEGM LLPPPSVQWN HNYDGE GGD VSLWSY-
    ***** ** * ****
181 : SLLDNMAEGM LLPSPSVQWN YNFDVE GDD VSLWSY*

```

+++++

```

Sequence 1      : DREB1B.aa
Size            : 213
Matching Position : 1 - 213

Sequence 2      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224

```

## Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
* N+         : 2

Matching      : 65.93 [%]
Weight       : -56

```

```

1 : MNSF-SAF-- SEMFGSDYEP QGGD---YCP TLATSCPKKP AGRKKFRETR HPIYRGVRQR
   ** * * * *
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVRQR

55 : NSGKVVSEVR EPNKKTRIWL GTFQTAEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    *****
61 : NSGKVVSEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE

115 : STCAKDIQKA AAEALAFQD ETCDDTTTNNH GLDMEE---T MVE---AIYTP EQSEGAFYMD
    ** * **** * * *
121 : TTCPEIKQKA ASEAAAFQN ET-TTEGSKT AAEAEAAAGE GVREGERRAE EQNGGVFYMD

170 : EETMFGMPTL LDNMAEGMLL PPSPVQWNHN YDGE GGD VSLWSY--Y
    * ****
180 : DEALLGMPNF FENMAEGMLL PPPEVGWNHN -DFDGVGDVS LWSFDE

```

Fig. 3-5

0046368

+++++

Sequence 1 : DREB1B.aa  
 Size : 213  
 Matching Position : 1 - 213

Sequence 2 : DREB1E.aa  
 Size : 181  
 Matching Position : 1 - 181

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 44.95 [%]  
 Weight : 34

1 : MNSFSAFSEM FGSDYEPQGG DYCP TLATSC PKKPAGRK KF RETRHPIYRG VRQRNSGKWV  
 \* \* \* \* \*  
 1 : M-----E NDDITVAEMK PKKRAGRRIF KETRHPIYRG VRRRDGDKWV  
 61 : SEVREPNNKT RIWLGTFQTA EMAARAH DVA ALALGRSAC LNFADSAWRL RIPESTCAKD  
 \*\*\*\*\* \* \* \* \* \*  
 43 : CEVREPIHQR RVWLGTYPTA DMAARAH DVA VLALGRSAC LNFSDSAWRL PVPASTDPDT  
 121 : IQKAAAEAL AFQDETCDDT TTNHGLDMEE TMVEAIYTP E QSEGA FYMDE ETMFGMPTLL  
 \* \* \* \* \* \* \* \* \* \*  
 103 : IRRTAEEAE MFRPPEFSTG IT-----VLPS ASE---FDTSD EGVAGMMML  
 181 : DNMAEGMLLP PPSVQWNHN---YDGE-GD GDVSLWSY  
 \* \* \* \* \*  
 147 : ---AEEPLMS PPRS YIDMNT SVYVDEEMCY EDLSLWSY

+++++

Sequence 1 : DREB1B.aa  
 Size : 213  
 Matching Position : 1 - 213

Sequence 2 : DREB1F.aa  
 Size : 209  
 Matching Position : 1 - 209

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 43.72 [%]  
 Weight : 43

1 : MNSFSAFSEM FGSDYEPQGG DYCP TLATSC PKKPAGRK KF RETRHPIYRG VRQRNSGKWV  
 \*\* \* \* \* \* \*  
 1 : MN-----NDDIILAEMR PKKRAGRRVF KETRHPIYRG IRRRDGDKWV  
 61 : SEVREPNNKT RIWLGTFQTA EMAARAH DVA ALALGRSAC LNFADSAWRL RIPESTCAKD  
 \*\*\*\*\* \* \* \* \* \*  
 43 : CEVREPTHQR RIWLGTYPTA DMAARAH DVA VLALGRSAC LNFADSAWRL PVPESNDPDV  
 121 : IQKAAAEAL AF---QDETC DTTTTNHGLD MEETMVEAIY TPEQSE----GAFYMDDE

Fig. 3-6

0046368

```

      *   *   *   *   *   *   *   *
103 : IRRVAAEAAE MFRPVDLESG ITVLPCAGDD VDLGFGSGSG SGSGSEERNS SSYGFGDYEE
      * *   * * * * *   *   *   *   *
172 : TMFGMPTLLD NMAEGMLLP P-----SVQ WNHNYDGE-G DGDVSLWS-- Y
      * *   * * * * *   *   *   *   *
163 : VSTTMMRL-- --AEGPLMSP PRSYMEDMTP TNVYTEEMC YEDMSLWSYR Y

```

+++++

```

Sequence 1      : DREB1C.aa
Size            : 216
Matching Position : 1 - 216

```

```

Sequence 2      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 65.33 [%]
Weight       : -59

```

```

1 : MNSF-SAF-- SEMFGSDYES PVSSGGDYSP KLATSCPKKP AGRKKFRETR HPIYRGVRQR
  ** * * * *   ** * * * *   ** * * * *   ** * * * *   ** * * * *
1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSK KLASSCPKKR AGRKKFRETR HPIYRGVRQR

```

```

58 : NSGKWVCELR EPNKKTRIWL GTFQTAEMAA RAHDVAAIAL RGRSACLNFA DSAWRLRIPE
    ***** * ***** * * * * * * * * * * * * * * * * * * * * * *
61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE

```

```

118 : STCAKEIQKA AAEEALNFQ- ---DEMCHMT TDAHGLDMEE TLVEAIYTPE QSQDAFYMDE
    ** * * * * * * * *   *   *   *   *   *   *   *   *   *   *
121 : TTCPEIQKA ASEAAAFQN ETTTEGSKTA AEAEAAAGEG VREGERRAEE QNGGVFYMD

```

```

174 : EAMLGMSLL DNMAEGMLLP SPSVQWNYNF DVEGDDDVSL WS--Y
    ** * * * * * * * * * * * * * * * * * * * * * *
181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHN- DFDGVGDVSL WSFDE

```

+++++

```

Sequence 1      : DREB1C.aa
Size            : 216
Matching Position : 1 - 216

```

```

Sequence 2      : DREB1E.aa
Size            : 181
Matching Position : 1 - 181

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 43.24 [%]
Weight       : 42

```

Fig. 3-7

0046368

```

1 : M-NSFSAFSE MFGSDYESPV SSGDYSPL ATSCPKKAG RKKFRETRHP IYRGVRQRNS
   * * * * *
1 : MENDDITVAE M----- ---KPKKRAG RRIFKETRHP IYRGVRRRDG

60 : GKWVCELREP NKKTRIWLGT FQTAEMAARA HDVAAIALRG RSACLNFAADS AWRLRIPEST
     *****
39 : DKWVCEVREP IHQRRVWLGT YPTADMAARA HDVAVLALRG RSACLNFSDS AWRLPVPAST

120 : CAKEIQKAAA EAALNFQDEM CHMTTDAHGL DMEETLVEAI YTPESQDAF YMDEEAMLGM
      * ** * * *
99 : DPDTIRRTAA EAA----EM FRPPEFSTG- ----- ITVLPSASEF DTSDEGVAGM

180 : SLLDNMAEG MLLPSPSVQW NYNFDVEGD- ----DDVSLW SY
      * ** * *
143 : MMRL---AEE PLMSPPRSYI DMNTSVYVDE EMCYEDLSLW SY
  
```

+++++

```

Sequence 1      : DREB1C.aa
Size            : 216
Matching Position : 1 - 216
  
```

```

Sequence 2      : DREB1F.aa
Size            : 209
Matching Position : 1 - 209
  
```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 41.88 [%]
Weight           : 52
  
```

```

1 : MNSFSAFSEM FGSDYESPVS SGGDYSPLA TSCPKKPAGR KKFRETRHPI YRGVRQRNSG
   ** * * * *
1 : MN----- ---NDDIILA EMRPKKRAGR RVFKETRHPV YRGIRRRNGD

61 : KWVCELREP NKKTRIWLGT FQTAEMAARA HDVAAIALRG RSACLNFAADS AWRLRIPESTC
     *****
40 : KWVCEVREP IHQRRVWLGT YPTADMAARA HDVAVLALRG RSACLNFSDS AWRLPVPAST

121 : AKEIQKAAA EAALNF--QDE MCHMT----- TDAHGLDMEE TLVEAIYTPY --QSQDAFYM
      * ** * *
100 : PDVIRRVAAE AAEMFRPVDL ESGITVLPCA GDDVDLGFSG GSGSGSGSEE RNSSSYGFSGD

172 : DEEAMLGMS LLDNMAEGML LPSP----- -SVQWNYNFD VEGDDDVSLW S--Y
      * * * *
160 : YEEVSTTMMR L----AEGPL MSPPRSYMED MTPTNVYTEE EMCYEDMSLW SYRY
  
```

+++++

```

Sequence 1      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224
  
```

```

Sequence 2      : DREB1E.aa
Size            : 181
Matching Position : 1 - 181
  
```

Matching Condition.



Fig. 3-8

0046368

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 42.17 [%]
Weight       : 50

```

```

1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVRQR
  *      *
1 : MENDDIT--- ----- -VAEMKPKKR AGRRIFKETR HPIYRGVRRR

```

```

61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    ***** ** * ** * ** * ***** ** ***** *
37 : DGDKWVCEVR EPIHQRRVWL GTYPTADMAA RAHDVAVLAL RGRSACLNFS DSAWRLPVPA

```

```

121 : TTCPKETQKA ASEAAAFQN ETTTEGSKTA AEAEAAAGEG VREGERRAE QNGGVFYMD
    * * * * * ** * * * * *
97 : STDPDTIRRT AAEEAEF--- ----- RPPEFSTGIT Y---LPSASE -----FDTSD

```

```

181 : EALLGMPNFF ENMAEGMLLP PPEVGWNHND FDGV----- GDVSLWSFDE
    * ** ** * ** * * * * *
137 : EGVAGM---M MRLAEPLMS PPRS IDMNT SVYVDEEMCY EDLSLWS---Y

```

+++++

```

Sequence 1      : DREB1D.aa
Size            : 224
Matching Position : 1 - 224

```

```

Sequence 2      : DREB1F.aa
Size            : 209
Matching Position : 1 - 209

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 42.13 [%]
Weight       : 49

```

```

1 : MNPFYSTFPD SFLSISDHRS PVSDSSECSP KLASSCPKKR AGRKKFRETR HPIYRGVRQR
  **
1 : MN----- -NDDI ILAEMRPKKR AGRRVFKETR HPVYRGIRRR

```

```

61 : NSGKWVCEVR EPNKKSRIWL GTFPTVEMAA RAHDVAALAL RGRSACLNFA DSAWRLRIPE
    * ***** ** ***** ** ** * ***** ** ***** **
37 : NGDKWVCEVR EPTHQRRVWL GTYPTADMAA RAHDVAVLAL RGRSACLNFA DSAWRLPVPE

```

```

121 : TTCPKETQKA ASEAAAFQN ETTTEG--SK TAAEAEAAAG EGVREG-ERR AEEQNGGVFY
    * * * * * * * * * * *
97 : SNPDVIRRV AAEEAEFRP VDLESGITVL PCAGDDVDLG FGSGSGSGSG SEERNSSSYG

```

```

178 : MDDEALLGMP NFFENMAEGM LLPPP----E VGWNHN---- DFDGVGDVSL WSFDE
    * * * * * * * * * *
157 : FGD--YEEVS TTMMRLAEGP LMSPPRSYME DMTPTNVYTE EEMCYEDMSL WSYRY

```

+++++

Fig. 3-9

0046368

Sequence 1 : DREB1E.aa  
Size : 181  
Matching Position : 1 - 181

Sequence 2 : DREB1F.aa  
Size : 209  
Matching Position : 1 - 209

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 69.38 [%]  
Weight : -71

```

1 : MENDDITVAE MKPKKRAGRR IFKETRHPIY RGVRRRDGDK WVCEVREPIH QRRVWLGTY
  * **** ** * ***** ***** * ** *** ** ***** * *** *****
1 : MNNDIILAE MRPKKRAGRR VFKETRHPIY RGVRRRDGDK WVCEVREPIH QRRVWLGTY

61 : TADMAARAHD VAVLALGRS ACLNFSDSAW RLPVPASTDP DTIRRTAAEA AEMFRPPEFS
  ***** ***** ***** ***** * ** * *** *****
61 : TADMAARAHD VAVLALGRS ACLNFADSAW RLPVPESNDP DVIRRVAAEA AEMFRPVDLE

121 : TGITVLP--- -----SASEFD TS-----D EGVAGMMML AEEPLMSPPR
  ***** * ** * * * *****
121 : SGITVLPAG DDVDLGFSG SGSGSGSEER NSSYGFSDY EEVSTTMMML AEGPLMSPPR

157 : SY-IDM-NTS VYVDEEMCYE DLSLWS--Y
  ** ** * ** ***** * *****
181 : SYMEDMTPTN VYTEEEMCYE DMSLWSYRY
  
```

Fig. 4-1

0010181

```

+++++
Sequence 1      : DREB2A.nuc
Size           : 1008
Matching Position : 1 - 1008

Sequence 2      : DREB2B.nuc
Size           : 993
Matching Position : 1 - 993

Matching Condition.

Matches        : -1
Mismatch       : 1
Gaps           : 1
* N+           : 2

Matching       : 63.40 [%]
Weight         : -222

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
    ***** * * **** * * * **      *** * * *
1 : ATGGCTGTAT ATGAACAAAC CGG----- AACCGAGCA- ----- GCCGAAGAAA

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
    ***** * * .*** * *** ** ***** * ** **** * *
43 : AGGAAATCTA GGGCTCGAGC AGGTGGTTTA ACGGTGGCTG ATAGGCTAAA GAAGTGGAAA

121 : GAGTATAACG AGACCGTAGA AG----AAGT TTCTACCAAG AAGA----- ----GGAAA
    ***** **** * * * * * * * * * * * * * * * * * *
103 : GAGTACAACG AGATTGTTGA AGCTTCGGCT GTTAAAGAAG GAGAGAAACC GAAACGCAAA

166 : GTACCTGCGA AAGGGTCGAA GAAGGGTTGT ATGAAAGGTA AAGGAGGACC AGAGAATAGC
    ** ***** ***** ** ***** ***** ** ***** **
163 : GTTCCTGCGA AAGGGTCGAA GAAAGGTTGT ATGAAGGTA AAGGAGGACC AGATAATTCT

226 : CGATGTAGTT TCAGAGGAGT TAGGCAAAGG ATTTGGGGTA AATGGGTTGC TGAGATCAGA
    * ***** * ***** ** ***** ***** ***** *****
223 : CACTGTAGTT TTAGAGGAGT TAGACAAAGG ATTTGGGGTA AATGGGTTGC AGAGATTCCA

286 : GAGCCTAATC GAGGTAGCAG GCTTTGGCTT GGTACTTTCC CTAAGCTGCTA AGAAGCTGCT
    ** ** * * * * * * * * * * * * * * * * * * * * *
283 : GAACCGAAAA TAGGAACTAG ACTTTGGCTT GGTACTTTTC CTACCGCGGA AAAAGCTGCT

346 : TCTGCTTATG ATGAGGCTGC TAAAGCTATG TATGGTCCTT TGGCTCGTCT TAATTTCCCT
    ** ***** **** * * * * * * * * * * * * * * * *
343 : TCCGCTTATG ATGAAGCGGC TACCGCTATG TACGGTTCAT TGGCTCGTCT TAATTTCCCT

406 : CGGTCTGATG CGTCTGAGG TACGAGTACC TCAAGTCAGT CTGAGGTGTG TACTGTTGAG
    * ***** * * * * * * * * * * * * * * * * * *
403 : CAGTCTGTTG GGTCTGAGT TACTAGTACG TCTAGTCAAT CTGAGGTGTG TACGGTTGAA

466 : A----- ---CTCCTGG TTGTGTTTAT GTGAAAACAG AGGATCCAGA TTGTGAATCT
    * * * * * * * * * * * * * * * * * * * * *
463 : AATAAGGCGG TTGTTTGTGG TGATGTTTGT GTGAAGCATG AAGATACTGA TTGTGAATCT

514 : AAACCTTT-- CTCCG---GT GGA--GTGGA GCCGATGTAT TGT----- --CTGGAGAA
    ** ** * * * * * * * * * * * * * * * * *
523 : AATCCATTTA GTCAGATTTT AGATGTTAGA GAAGA-GTCT TGTGGAACCA GGCCGGACAG

558 : TGGTGCGG-A AGAGATGAAG AGAGGTGTT- AAAGC-GGAT AAGCATTGGC TGAGCGAGTT
    * * *** ** * * * * * * * * * * * * * * *

```

Fig. 4-2

0010181

```

582 : TTGCACGGTT GGACATCAAG ATATGAATTC TTCGCTGAAT TACGATTTGC TGTTAGAGTT
615 : TGAACATAAC TATTGGAGTG ATATTCTGAA AGAGAAAGAG AAACAGAAGG AGCAAGGGAT
    *** ** * ***** * * *** * ***** **** **** ** ** *
642 : TGAGCAGCAG TATTGGGGCC AAGTTTTCGA GGAGAAAGAG AAACCGAAGC AGGAA-GAAG
675 : TGTAGAAAC- CTGTCAGCAA CAACAGCAGG ATTCGCTATC TGTTGCAGAC TATGGTTGGC
    * *** ** ***** ** * *** * *** * * **** ** * ** **
701 : AGGAGATACA GCAACAGCAA CAGGAACAGC AACAGC-AAC AGCTGCA-AC -CGGATTTGC
734 : CCAATGATGT GGATCAGAGT --CACTTGA TTCTTCAGAC ATGTTTGATG TCGATGAG-C
    * ** ** *** * ** ***** *** ** ** * ** *** ** *
758 : TTAATGTTGC AGATTACGGT TGGCCTTGG- -TCTAATGAT ATTGTAAAT- --GATCAGAC
791 : TTCTACGTGA CCTAA--ATG GCGACGATGT GTTTGCAGGC TTAAATCAGG ACCGGTACCC
    **** * ***** * ** *** * ** * * * * * * *
813 : TTCTTGGGAT CCTAATGAGT GCTTTGATAT TAATGAACTC CT---TGGAG ATTTGAA---
849 : GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT CAACAAAGTG GTTTTGATCC
    **** ** *** * * * ** * ** * **** * ** * **
867 : --TGAACCTG GTCCCATCA G---AGCCAA GACCAA---- -AACCAGTA AAT----TCT
909 : GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC GAGGGAAAGG ATGGTAATGG
    * * * ** * * * ** * * ** * * * * * * *
913 : GGT----- --AGTTATG ATTTGCATCC GCTTCATCTC GAGCCACAGC ATGGTCACG-
969 : ATTCTTCGAC GACTTGAGTT ACTTGGATCT GGAGAACTAA
    *** * * ***** *** ** * *
962 : --AGTTCAAT GGTTCAGTT -----CTCT GGATATTTGA
  
```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008
  
```

```

Sequence 2      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026
  
```

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
* N+         : 2

Matching      : 55.22 [%]
Weight       : -8
  
```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAG- AAACAGAACA CAAATTGATA CATCGAGGAA
    ** ** ** ***** * **** * ** ** *** ****
1 : AT-GCCGT-- ----- CGGAGATTGT TGACAGGAA- -AAG--GAAG TCTCGTGGAA
60 : AAGGAAATCT AGAAGTAGAG GTGACGGTAC TACTGTGGCT GAGAGATTAA AGAGATGGAA
    * ** ** * ** * *** * ** * * * * * * **
44 : CACGAGATGT AGCTG-AGAT TCTAAGGCAA TGGAGAGAGT ---ACAATGA GCAGATTGAG
120 : AGAGTATAAC GAGACCGTAG AAGAAGTTTC TACCAAGAAG AGGAAAG-TA CCTGCGAAAG
    ** ** * ** * * * ** * * ** ***** *** * ****
100 : GCAGAATCTT G-TATCGATG GTGGTG-GTC CAAAATCAAT CCGAAAGCCT CCTCCAAAG
  
```

Fig. 4-3

-0010181

```

179 : GGTCAAGAA GGGTTGTATG AAAGGTAAAG GAGGACCAGA GAATAGCCGA TGTAGTTTCA
    * *** ** ***** ***** * ***** ** * *** * *
158 : GTTCGAGGAA GGGTTGTATG AAAGGTAAAG GTGGACCTGA AAACGGGATT TGTACTATA

239 : GAGGAGTTAG GCAAAGGATT TGGGGTAAAT GGGTTGCTGA GATCAGAGAG CCTAATCGAG
    ***** ** **** ***** ***** ***** * *** * ***
218 : GAGGAGTTAG ACAGAGGAGA TGGGGTAAAT GGGTTGCTGA GATCCGTGAG CCAGACGGAG

299 : GTAGCAGGCT TTGGCTTGGT ACTTCCCTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
    ** *** * ***** ** ***** * * * * * * ***** *
278 : GTGCTAGGTT GTGGCTCGGT ACTTCTCCA GTTCATATGA AGCTGCATTG GCTTATGACG

359 : AGGCTGCTAA AGCTATGTAT GGTCTTTGG CTCGTCTTAA T-TTCCC--- -----TC
    **** ** ** ***** ** ***** * * * * * * ***** **
338 : AGGCGGCCAA AGCTATATAT GGTCACTCTG CCAGACTCAA TCTTCCCGAG ATCACAATC

407 : GGTCTGATGC GTCTGAGG-- -TTACGAGTA CCTCAAG-TC AGTCTGAGGT GTGTACTGTT
    * *** * * * * * * * * * * * * * * * * * * * *
398 : GCTCTTCTTC GACTGCTGCC ACTGCCACTG TGTGAGGCTC GGT-TACTGC ATTTTCTGAT

463 : GAGACTCCTG GTTGTGTTCA TGTGAAAACA GAGG---ATC CAGATTGTGA ATCTAAACCC
    ** ** * ***** * ** * * * * * * * * * * * * *
457 : GAATCTGAAG TTTGTGCACG TGAGGATACA AATGCAAGTT CAGGTTTGT- GTC---AGGT

520 : TTCTCCGGTG GAGTGGAGCC GATG--TATT GTCTGGAGAA TGGTGCAGAA GAGATGAAGA
    * * * * * * * * * * * * * * * * * * * * *
513 : GAAACTAGAG GATTGTAG-C GATGAATATG TTCTCTTAGA TAGTCTCAG TGTATTAA-A

578 : GAGGTGTTAA AGCGGATAAG CATTGGCTGA GCGAGTTTGA ACATAACTAT TGGAGTGATA
    ***** * * * * * * * * * * * * * * * * * * *
571 : GAGGAGCTGA A-AGGAAAAG -AGGAAGTGA GGGA---AGA ACATAACT-T GGCTGTTGGT

638 : TTCTGAAAGA GAAAGAGAAA CAGAAGGAGC AAGGGATTGT AGAAACCTG- -TCAGCAACA
    ** *** ** * * * * * * * * * * * * * * * * *
625 : TTTGGAATTG GACAG-GACT C-GAAAAGG- --GAGACTTT GGATGCTTGG TTGATGGGAA

696 : ACAGCAGGAT TCCTATCTG TTGCAGACTA TGGT-TGGCC CAA-----TG ATGTGGATCA
    * *** * * * * * * * * * * * * * * * * * *
680 : ATGGCAATGA ACAAGAACCA TTG--GAGTT TGGTGTGGAT GAAACGTTTG ATATTAAT--

750 : GAGTCACTTG GATTCTTCA- -GACATGTTT GATGTCGATG AGCTTCTACG TGACCTAAAT
    *** * * * * * * * * * * * * * * * * * * *
736 : GAGCTATTGG GTATATTAAA CGACAACAAT G-TGTC--TG ---GTC-AAG AGAC---AAT

808 : GGCG-ACGAT GTGTTTGCAG GCTTAAATCA GGACCGGTAC CCGGGGAACA GTGTTGCCAA
    * * * * * * * * * * * * * * * * * * * *
786 : GCAGTATCAA GTGGATAGAC ACCCAAAT-- -TTCAGTTAC C----AAACG CAGTTTCCAA

867 : CGGTTTCATAC AGGCCCCGAGA G--TCAACAA AGTGGTTTTG ATCCGCTACA AAGCCTCAAC
    *** ** * * * * * * * * * * * * * * * *
839 : --ATTCTAAC TTGCTCGGGA GCCTCAACCC TATGGAGAT- -TGCTCAACC AGGAGTTGAT

925 : TACGGAATAC CTCCGTTTCA GCTC---GA- --GGGAAAGG ATGGAATGG ATT-----
    ** *** * * * * * * * * * * * * * * * *
895 : TATGGATGTC CTTATGTGCA GCCCAGTGAT ATGGAGAAGT ATGGTATTGA TTTAGACCAT

972 : -----CTTCG ACGA-CTTGA GTT-----AC TTGGATCT-- --GGAGA--- -----
    *** * * * * * * * * * * * * * * * *
955 : CGCAGGTTCA ATGATCTTGA CATACAGGAC TTGATTTTG GAGGAGACAA AGATGTTTCAAT

```

Fig. 4-4

0010181

1004 : -----AC-T AA  
 \*\* \* \*\*  
 1015 : GGATCTACAT AA

+++++

Sequence 1 : DREB2A.nuc  
 Size : 1008  
 Matching Position : 1 - 1008

Sequence 2 : DREB2D.nuc  
 Size : 621  
 Matching Position : 1 - 621

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 44.17 [%]  
 Weight : 226

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA  
 \*\*\*  
 1 : ATG-----TCATCC ATAGAG-----  
 61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA  
 \* \* \*\*\*\*\* \*\*\* \*\*\* \*\* \*\*\* \* \*\*\* \*\*\*  
 16 : -----CCA AAAGTA---A TGATGGT---TGGTGCT---AATAA-----GAA-  
 121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TGCGAAAGGG  
 \* \*\*\*\* \* \*\*\*\*\* \*\*\*\*\* \* \* \*  
 48 : ---ACAACG A-ACCGT---CCAAAG---C T-----AGT  
 181 : TCGAAGAAGG GTTGATGAA AGGTAAATGG GGACCAGAGA ATAGCCGATG TAGTTTCAGA  
 \*\*\*\* \* \* \*\*\*\*\* \*\*\* \*\*\*\*\* \*\*\*\*\* \* \* \* \*\* \* \* \* \*  
 70 : TCGAGGAAAG GTTGATGAG AGGAAAAGGT GGACCCGATA ACGCGTCTTG CACTTACAAA  
 241 : GGAGTTAGGC AAAGGATTTG GGGTAAATGG GTTGCTGAGA TCAGAGAGCC TAATCGAGGT  
 \*\* \*\*\*\*\*  
 130 : GGTGTTAGAC AACGCACTTG GGGCAAATGG GTCGCTGAGA TCCGCGAGCC TAACCGAGG-  
 301 : AGC-AGGCTT TGGCTTGTA CTTTCCCTAC TGCTCAAGAA GCTGCTTCTG CTTATGATGA  
 \*\*\*  
 189 : AGCTCGTCTT TGGCTCGGTA CTTTCGACAC CTCCCGTGAA GCTGCCTTGG CTTATGACTC  
 360 : GGCTGCT--A AAGCTATGTA TGGTCCTTTG GCTCGTCTTA ATTCCCTCG GTCTGATGCC  
 \*\* \*\*\* \*\*\*\*\*  
 249 : CGCAGCTCGT AAGC--TCTA TGGGCTGAG GTCATCTCA ACCTCCCT--  
 418 : TCTGAGGTTA CGAGTACCTC AAGTCAGTCT GAGGTGTGTA CTGTTGAGAC TCCTGGTTGT  
 \*\*\*\*\* \*\*  
 295 : -----GAGT-CCTT AA-----GAAGT---TA C-----CCT-----  
 478 : GTTCATGTGA AAACAGAGGA TCCAGATTGT GAATCTAAAC CCTTCTCCGG TGGAGTGGAG  
 \* \*\*\*\*  
 316 : -----A AAACGGCG-----TCGTCTCCGG CG-----T  
 538 : CCGATGTATT GTCTGGAGAA TGGTGGGAA GAGATGAAGA GAGGTGTTAA AGCGGATAAG  
 \*\*  
 338 : CCCA-----GACTACCA AGCAGC-----AACA CCGGTG-----GAAAAAG

Fig. 4-5

0010181

```

598 : CATTGGCTGA GCGAGTTTGA ACATAACTAT TGGAGTGATA TTCTGAAAGA GAAAGAGAAA
      ** ** * **** * ***          * * ***      *** * ** ****
375 : CA---GC--A GCGACTCTGA -----GT CGCCGTG--- TTC----ATC CAACGAGA--

658 : CAGAAGGAGC AAGGGATTGT AGAAACCTGT CAGCAACAAC AGCAGGATTC GCTATCTGTT
      * * *      *** *** **          ** ** **** * ****
413 : ---TGTATC A-----TGT GGAAGAGTG- -----AC AG-AGGA--- GATATC----

718 : GCAGACTATG GTTGGCCCAA TGATGTGGAT CAGAGTCACT TGGATTCTTC AGACATGTTT
      *** *** ** * ** ***** * * *
447 : -----ATG-GGAG CATATAAAGC TGGATT-TGC CG-----GT

778 : GATGTCGATG AGCTTCTACG TGACCTAAAT GGCGACGATG TGTTCGAGG CTAAATCAG
      *** **** * ****          * * ** ** ** *      * * ** ***
477 : AATG--GATG A--TTCT--- --TCAATAT GG---GAAG -----AAG CTACAAT---

838 : GACCGGTACC CGGGGAACAG TGTTGCCAAC GTTCATACA GGCCCGAGAG TCAACAAAGT
      ** **      ***          ** *** ***** * **      * * **
513 : -GTCGTTA-- ---GGA----- --TTCCATG GTTCATGAA GG-----AGATAAT

898 : GGTTCGATC' CGCTACAAAG CCTCAACTAC GGAATACCTC CGTTTCAGCT CGAGGGAAAG
      * * ** ** * *          ***** * ***** * *
550 : GATATTTCTC GGTT----- --TGATACTTG TATTTCCGGT -----G

958 : GATGGTAATG GATTCTTCGA CGACTTGAG- TTAATTGGAT CTGGAGAACT AA
      * *      ***** * *** * ** *** **      * *
584 : GCT-----ATTCT----- --AATTGGGA TTCCTTTCAT TCCCCACTTT GA

```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008

```

```

Sequence 2      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

## Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
* N +        : 2

Matching      : 49.90 [%]
Weight       : 128

```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAAT-----T GATACATCGA
    **** *      * ** ***      *** ** ***** * *      * * * ***
1 : ATGGAA---A AGGA--AGAT AACGGATCGA AACAGAGCTC CTCTGCTTCT GTTGTATCCT

56 : GGAAAAGGAA ATCTAGAAGT AGAGGTGACG GTACTACTGT GGCTGAGAGA TTAAAGAGAT
    ** ***      **** *** *** * *      * ** ** * ** *** *****
56 : CGAGAAG--- ---ACGAAGA AGA-GTG--G TTGAGCCAGT GGAAGCGACG TTACAGAGAT

116 : GGAAAGAGTA TAACGAGACC GTAGAAGAAG TTTCTACCAA GA-AGAGGAA AGTACCTGCG
    **          ***      ***** * * ** ** * *      * * ** **
107 : GG-----GAG--- ---GAAGAAG GAT-TGGCGA GAGCTCGTAG GGTTCAGGCC

175 : AAAGGGTCGA AGAAGGGTTG TATGAAAGGT AAAGGAGGAC CAGAGAATAG CCGATGTAGT

```

Fig. 4-6

```

                                0010181
148 : ***** **** * **** * **** * **** * **** * **** * **** *
      AAAGGTTCTGA AGAAAGGTTG TATGAGAGGA AAAGGTGGAC CAGAGAATCC TGTGTTGTCGG

235 : TTCAGAGGAG TTAGGCAAAG GATTGCGGT AAATGGGTTG CTGAGATCAG AGAGCCTAAT
      ** ***** * ** * ***** * ***** ***** ***** * ** **
208 : TTTAGAGGTG TTCGACAAAG GGTGTTGGGG AAATGGGTTG CTGAGATACG TGAACC----

295 : CGAGGTAGCA GGCTTTGGCT TGGTACTTTC CCTACTGCTC AAGAAGCTGC TTCTGCTTAT
      ** ** * * **** * * *** * * ** * ** ** ****
264 : --AGTGAG-- ----TCACCG TGGTGCAAAC TCTAGT-CGT AGTAAACGGC TTTGGCTTGG

355 : GATG-AGGCT GCTAAAGCTA TGTATGGTCC TTTGGCTCGT CTTAATTTCC CTCGGTCTGA
      * * *** ** **** * * * *****
315 : CACGTTTGCT ACTGCAGCT- --GAAGCTGC TTTGGCT--- -----

414 : TCGCTCTGAG GTTACGAGTA CCTCAAGTCA GTCTGAGGTG TGTACTGTTG AGACTCCTGG
      * ** * ** * * **** ****
349 : TACGACAGA- GCTGCTAGT- ----GTCA ----- TGTAC----- GGAC-CCT--

474 : TTGTGTTTAT GTGAAAACAG AGGATCCAGA TTGTGAATCT AAACCTTCT CCGGTGGAGT
      ** * **** ** * *** ** **** **
383 : -----AT G----- ----CCAG- --GT-----T AAA---TTTC CCGGAAGATT

534 : GGAGCCGATG TATTGTCTGG AGAATGGTGC GGAAGAGATG AAGA-GAGGT GTTAAAGCGG
      * * ** ** **** ***** * * * ** * ** *
410 : TGGG----- --TG--GG GGAA----- GGAAGA-AGG ACGAGGAGGC GGAAAGTTGC

593 : ATAAGC-ATT GGCTGAGCGA GTTTGAACAT AAC---TATT GGAGTGATAT TCTGAAAGAG
      * ** *** ** ** * **** * * ** * ** ***** ***** *
451 : GGAGGCTATT GGTG---GA AACT-AACAA AGCCGGTAAT GGCGTGAT-- --TGAACGG

649 : AAAGAGAAAC AGAAGGAGCA AGGGATTGTA GAAACCTGTC AGCAACAACA GCAGGATTCG
      ** * * ** ** * * **** * * **** * * **
503 : AAGGTGAAAA AGA-----CT A-----TGTA G----- -TCTACAA-- --TGAAGACG

709 : CTATCTGTTG CAGACTATGG TTGGCCCAAT GATGTGGATC AGAGTCACTT GGATTCTTCA
      **** * * ***** ** ** * * ** *** ** **
539 : CTAT----- ----TGAGC TTGGCC--AT GA-----C A-AG--ACTC AGAATCCT--

769 : GACATGTTTG ATGTCGATGA GCTTCTACGT GACCTAAATG GCGACGATGT GTTTGCAGGC
      *** ** ** **** * ** ** * * *
574 : ---ATGACTG AT---AATGA AAT---AGT GAAC----- --CCA--- ----GCAG--

829 : TTAAATCAGG ACCGGTACCC GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT
      * ***** ** * ** **** ** * ** **** * *
605 : TGAAATCAG- --AGGAA--- -GGTTACAGC TATG--ATCG ATTCAAATTG G-----

889 : CAACAAAGTG GTTTTGATCC GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC
      * ** * * *** ** ** * *** * * ** **** ** * **
647 : --ATAACGGA TTGTTG---- --TATAA--- -TGAACCTC- --AAAGCTCC AGTT-ATCAC

949 : GAGGGAAAGG ATGGTAATGG ATTCTTCGAC GACTTGAGTT ACTTGGATCT GGAGAACTAA
      ***** * *** * * * **** * ***** * ***
691 : CAGGGA---G GTGG-ATTCG ATTC----AT ATTTTGAGTA TTTGAGAT-- ----TCTAG

```

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Sequence 1 : DREB2A.nuc  
 Size : 1008  
 Matching Position : 1 - 1008



Fig. 4-7

0010181

Sequence 2 : DREB2F.nuc  
 Size : 834  
 Matching Position : 1 - 834

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 48.48 [%]  
 Weight : 158

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
   ***                               ****
1 : ATGG-----AGAA-----ATC-----

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
   ***                               ** * ** *** * *****
12 : -----ATC-----CTC A---ATGAAA CA-ATGGAA-

121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TCGGAAAGGG
   33 : -----GAAGGGTCC TGC-----

181 : TCGAAGAAGG GTTGATGAA AGGTAAAGGA GGACCAGAGA ATAGCCGATG TAGTTTCAGA
   ***                               ***** ** *** * * * * * * * *
45 : TCG-----GGGTAAAGGC GGTCCACAAA ACGCTCTTTG TCAGTACCGT

241 : GGAGTTAGGC AAAGGATTGG GGGTAAATGG GTTGCTGAGA TCAGAGAGCC TAA-TCGAGG
   ***** ** * * * * * * * * * * * * * * * * * * *
88 : GGAGTCAGGC AAAGGACTTG GGGCAATGG GTGGCTGAGA TCAGAGAGCC CAAGAAGAGG

300 : TAGC-AGGCT TTGGCTTGGT ACTTTCCTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
   ** ** * * * * * * * * * * * * * * * * * * *
148 : --GCAAGACT TTGGCTTGGC TCTTTCGCTA CAGCTGAAGA AGCAGCTATG GCTTATGATG

359 : AGGCTGC--T AAAGCTATGT ATGGTCCTTT GGCTCGTCTT AATTTCCCTC GGTCTGATGC
   ***** * * * * * * * * * * * * * * * * * * *
206 : AGGCTGCCTT GAAAC--TCT ATGGGCACGA CGCATACCTC AACTTACCTC -ATCTTCAGC

417 : GTCTGAGGTT ACGAGTACCT CAAGTCAGTC TGAGGTGTGT ACTGT-TGAG ACTCCTGGTT
   * * * * * * * * * * * * * * * * * * *
263 : G-----GAAT ACAAG-ACCT ----TC--TC TGAG----TA ACTCTCAGAG GTTC--AAAT

476 : GTGTTTCATGT GAAACAGAG GATCCAGATT GTGAATCTAA ACCCTTCTCC GGTGGAGTG-
   * * * * * * * * * * * * * * * * * * *
305 : GGTACCT-- ----TCA-AG GA--AGTTT AT--ATCTAT GTTTCCTTCA TGTGGTATGC

535 : GAGCCGATGT ATTGTCTGGA GAATGGTGCG GAAGAGATGA AGAGAGGTGT-TAAAGCGGAT
   * * * * * * * * * * * * * * * * * * *
353 : TAAACG-TGA ATGCTC---A GCCTAGTGTT CACATAATCC AGCAAAGACT AGAAGAACTC

595 : AAGCATTGGC TGAGCGAGTT TGAACATAA- -CTATTGGAG T-GATATTCT GAAAGAGAAA
   *** * * * * * * * * * * * * * * * * * *
409 : AAGAA--AAC TG---GACTT TTATCTCAAT CCTATTCTTC TAGTTCTTCC TCCACCGAAT

652 : GAGAAAC-AG AAGGAGC--A AGGGAT-TGT AGA--AACCT GTCAGCAACA -ACAGCAGGA
   * * * * * * * * * * * * * * * * * * *
464 : CAAAACTAA TACTAGCTTT CTTGATGAGA AGACCAGCAA GGGAGAAACA GACAATATG-
```

Fig. 4-8

0010181

```

705 : TTCGCTATCT GTTG--CAG- ----ACTATG GTTGGCCCAA TGA-TGTGGA TC-AGAGTCA
      **** * * * * * ** * * * * * *** * * ** * *
523 : TTCG-AAGGT GGTGATCAGA AGAAACCAGA GATCGACC-- TGACCGAGTT TCTTCAGCAA

756 : CTTGGATTCT TCAGACATG- -TTTGATGTC GA-----TG AGCT-TCTAC GTGACCTAAA
      ** *** ** * * *** ** * ** ** * * *** * *
580 : CTAGGAATCT TGAAGGATGA AATGAAGCA GAACCAAGTG AGGTAGCAGA GTGTCATTCC

807 : TGGCGACGAT -GTGTTTGCA GGCTTAAATC AGGACCGGTA CCCGGGGAAC AGTG-TTGCC
      * * * * * *** * *** * *** ** * **** * * * *
640 : CCTCCACCAT GGAACGAGCA AGAAGAAA-C TGGA--AGTC CTTTCAGAAC TGAGAATTC

865 : AACGGTTCAT A-CAGGCCCG AGAGTCAACA AAGTGGTTTT GATCCGCTAC AAAGC--CTC
      * * * ** * * * ** *** * * ***** * * * * * * * *
697 : AGCTG-GGAT ACCCTGATCG AGATGCCAAG AAGTG----- AAACCACAAC TATGCAATTT

922 : AACTACGGAA TACCTCCGTT TCAGCT-CGA GGGAAAGGAT GGTAATGGAT TCTTC---GA
      *** * * * ** * * * **** ** ***** * *** ** ****
751 : GACTCCAGCA -ACTTCGG-- -AAGCTATGA TTTTGAGGAT G---ATGTAT CCTTCCCTTC

978 : CGACTTGAGT TACT-TGGAT CTGGAGAACT AA
      * * * **** *** ** * * *
804 : CATCTGGGAC TACTACGGAA GCTTAG-ATT GA

```

+++++

```

Sequence 1      : DREB2A.nuc
Size            : 1008
Matching Position : 1 - 1008

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches    : 1
Gaps         : 1
* N +        : 2

Matching      : 47.08 [%]
Weight       : 149

```

```

1 : ATGGCAGTTT ATGATCAGAG TGGAGATAGA AACAGAACAC AAATTGATAC ATCGAGGAAA
   ****
1 : ATGG-----

61 : AGGAAATCTA GAAGTAGAGG TGACGGTACT ACTGTGGCTG AGAGATTAAA GAGATGGAAA
     ** *
5 : -----AA G-----AA

121 : GAGTATAACG AGACCGTAGA AGAAGTTTCT ACCAAGAAGA GGAAAGTACC TGCGAAAGGG
     *** *
10 : GAGCA-----ACC-----TCCG GCCAAGAA-A CGAA---ACA TGGGGA--GA

181 : TCGAAGAAGG GTTGATGAA AGGTAAAGGA GGACCAGAGA ATAGCCGATG TAGTTTCAGA
     ** * * * * *
46 : TCTAGAAAAG GTTGCATGAA AGGTAAAGGC GGTCCAGAGA ACGCCACGTG TACTTTCCGT

241 : GGAGTTAGGC AAAGGATTTG GGTAAATGG GTTGCTGAGA TCAGAGAGCC TAATCGAGGT
     ***** ** *

```

Fig. 4-9

0010181

```

106 : GGAGTTAGGC AACGGACTTG GGGTAAATGG GTGGCTGAGA TCCGTGAGCC TAACCGTGGG
301 : AGCAGGCTTT GGCTTGGTAC TTTCCCTACT GCTCAAGAAG CTGCTTCTGC TTATGATGAG
    * * * * *
166 : ACTCGTCTCT GGCTCGGCAC GTTAAATACC TCGGTCGAGG CCGCCATGCC TTACGATGAA

361 : GCTGCTAAAG CTATGTATGG TCCTTTGGCT CGTCTTAATT TCCCTCGGT- CTGATGCGTC
    ** ***** * **** ** ** ** *** * *
226 : GCCGCTAAGA AACTCTATGG ACACGAGGCT AAACCTCAA-- ---CTTGGTG CACCCACAAC

420 : TGAGGTTACG AGTACCTCAA GTCAGTCTGA GGTGTGTAAT GTTGAGACTC CTGGTTGTGT
    ** **** * * * * *
281 : AACACAACA AGTA---GTA GTGA-ACAGA AACTTGTCTT TTTCTGGCCA CGGGTCGGGT

480 : TCATG----T GAAAACAGAG GATCCAGATT GTGAAT---C TAAACCCT-- TCT---CCGG
    ** * * * * *
337 : TCTTGGGCTT ATAATAAGAA GCTCGATATG GTTCATGGGT TGGACCTGG TCTCGGCCAG

528 : TGGAGTGGAG C-CGATG-TA TTGTCTGGAG A-ATGGTGGC GAAGAGATGA AGAGAGGTGT
    *** * * * * *
397 : GCAAGTTGTT CACGAGGTTT TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGA-TGATGA

585 : TAAAGCGGAT AAGC-AT-TG GCTGAGCGAG TTTGAACATA ACTATTGGAG TGATATTCTG
    * * * * *
456 : TCATAGTCAT AATCGATGTT CGTCTTCAAG -TGGTTCGAA TCT-TTGTG -GTTATTACC

643 : AAAGAGAAAG AGAAACAGAA GGAGCAAGGG ATTGTAGA-- ----AACCTG TCA--GCAAC
    ** * **** ** * * *
513 : TAA-ACAAAG TGATTCACAA -GATCAAGAG ACCGTTAATG CTACGACTAG TTATGGCGGT

695 : AACAGCAGGA TTCGCTAT-- ----CTGTTG CAGACTATGG TTGGCCCAAT GATGTGGATC
    * * * * *
571 : GAAGGCGGTG GTGGCTCTAC GTTAACGTTT TCGACCAATT TGAAACCAA GAATTTGATG

749 : AG--AGTCAC TTGATTCTT CA---GA--- ----CATGT TTGATGT--- -CGATGAGCT
    ** ** * * * *
631 : AGTCAGAATT ATGGATTATA CAATGGAGCT TGGTCTAGGT TTCTTGTGGG GCAAGAAAAG

792 : TCTACGTGAC CT-AAATGGC GACGATGTGT TTGCAGGCTT AAATCAGGAC CGGTACCCGG
    *** ** * * * *
691 : AAGACGGAAC ATGACGTGTC ATCGTCGTGT GGATCGTCGG ACAACAAGGA GAGTATGTTG

851 : GGAAC-AG-T GTTGCCAACG GTTCATACA- GGCCCGAGAG TCAACAAAGT GGTTTTGATC
    * * * * *
751 : GTTCCTAGTT GCGGCGGAGA GAGGATGCAT AGGCCG-GAG TTGGAAGAGC GAACAGGATA

908 : CGCTACAAAG CCTCAACTAC GGAATACCTC CGTTTCAG-- --CTCGA-GG GAAAGGATGG
    ** * * * *
810 : TTTGGAAATG GATGATCTTT TGGAGATTGA TGATTTAGGT TTGTTGATTG GCAAAAATGG

963 : -----T AATGGATTCT TCGACGACTT --GAGTTACT TGGATCTGGA GAACTAA
    *** * * *
870 : AGATTTCAG AATTGGTGT GTGAAGAGTT TCAACATCCA TGAATTG-- GTTCTGA
  
```

+++++

Sequence 1 : DREB2A. nuc  
 Size : 1008  
 Matching Position : 1 - 1008

Sequence 2 : DREB2H. nuc

Fig. 4-10

0010181

Size : 534  
 Matching Position : 1 - 534

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 39.41 [%]  
 Weight : 304

```

1 : ATG-GCAGTT TATGATCAGA GTGGAGATAG AACAGAAACA CAAATTGATA CATCGAGGAA
   *** ** * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGCCCAGGA AACG-GAAGT CTCGTG-----GAACA CGAGATGTAG CTGAGATTCT

60 : AAGGAAATCT AGA-AGTAGA GGTGACGGTA CTAAGTGGC TGAGAGATTA AAGAGATGGA
   ***** ** * * * * * * * * * * * * * * * * * * * * *
51 : AAGGAAATGG AGAGAGTACA -ATGA--GCA -GACCGAGGC ----AGATTC TTG-CATCGA

119 : AAGAGTATAA CGAGACCGTA GAAGAAGTTT CTACCAAGAA GAGGAAAGTA CCTGCGAAAG
   * * * * * * * * * * * * * * * * * * * * * * * * * * *
102 : TGGTG-----GTG GTTCAA-----AACCAATCC GA--AAGGCT CCTCCAAAC

179 : GGTGGAAGAA GGGTGTATG AAAGGTAAAG GAGGACCGA GAATAGCCGA TGTAGTTTCA
   * * * * * * * * * * * * * * * * * * * * * * * * * * *
143 : GTTCGAGGAA GGGTGTATG AAAGGTAAAG GTGGACCTGA AAATGGGATT TGTGACTATA

239 : GAGGAGTTAG GCAAAGGATT TGGGGTAAAT GGGTTGCTGA GATCAGAGAG CCTAATCGAG
   ***** ** * * * * * * * * * * * * * * * * * * * * *
203 : CAGGAGTTAG ACAGAGGACA TGGGGTAAAT GGGTTGCTGA GATCCGTGAG CCAGGCCGAG

299 : GTAGCAGGCT TTGGCTTGGT ACTTCCCTA CTGCTCAAGA AGCTGCTTCT GCTTATGATG
   ** * * * * * * * * * * * * * * * * * * * * * * * * * *
263 : GTGCTAAGTT ATGGCTCGGT ACTTCTCTA GTTCATATGA AGCTGCATTG GCTTATGATG

359 : AGGCTGCTAA AGCTATGTAT GGTCTTTGG CTCGTCTTAA TTTCCCTCGG TCTGATGCGT
   ***** * * * * * * * * * * * * * * * * * * * * * *
323 : AGGCTTCCAA AGCTAT-----TTA-----CGG TC-----AGT

419 : CTGAGGTTAC GAGTACCTCA AGTCAGTCTG AGGTGTGTAC TGTGAGACT CCTGGTTGTG
   *** * * * * * * * * * * * * * * * * * * * * * * * *
350 : CTG-----CCCG ACTCAATCT-----TCCAC TGCTGCCAC-----TGTG

479 : TTCATGTGAA AACAGAGGAT CCAGATTGTG AATCTAAACC CTTCTCCGGT GGAGTGGAGC
   * * * * * * * * * * * * * * * * * * * * * * * * *
384 : T-----CAGGCT C--GGTT-----AC-----

539 : CGATGTATTG TCTGGAGAAT GGTGCGGAAG AGATGAAGAG AGGTGTTAAA GCGGATAAGC
   ** * * * * * * * * * * * * * * * * * * * * * * *
398 : ---TGCATTT TCT-----GATGAA-----

599 : ATTGGCTGAG CGAGTTTGAA CATAACTATT GGAGTGATAT TCTGAAAGAG AAAGAGAAAC
   **** * * * * * * * * * * * * * * * * * * * * * *
414 : ----TCTGA--AGTTTG-----TGCACGTG A-----

659 : AGAAGGAGCA AGGAGTTGTA GAAACCTGTC AGCAACAACA GCAGGATTG CTATCTGTTG
   **** * * * * * * * * * * * * * * * * * * * * *
434 : -----GGAT-----ACAAAT GCA-----

```

Fig. 4-11

0010181

```

719 : CAGACTATGG TTGGCCCAAT GATGTGGATC AGAGTCACTT GGATTCTTCA GACATGTTTG
      *** * *** **          * * ** *** ** **          ****
447 : -AGA-TCTGG TT----- ---TTGGTC AGA-TCTCT- ---AACTTC-----

779 : ATGTCGATGA GCTTCTACGT GACCTAAATG GCGACGATGT GTTTCAGGC TTAAATCAGG
      ***          * * ** *****          **** **
477 : ---TCG----- ---CAT TTCCAAAATG ----- ---TTAAGTC---

839 : ACCGGTACCC GGGGAACAGT GTTGCCAACG GTTCATACAG GCCCGAGAGT CAACAAAGTG
      ** *          *** * ***          **
500 : -----CAAT -----AAC- -TGCAT----- -TG

899 : GTTTTGATCC GCTACAAAGC CTCAACTACG GAATACCTCC GTTTCAGCTC GAGGGAAAGG
      ***          ***          **          ***
514 : GTT-----AAG----- -TT----- -GGG-----

959 : ATGGTAATGG ATTCTTCGAC GACTTGAGTT ACTTGGATCT GGAGAACTAA
      * ***          ****
525 : -----GCGTT----- -ACTAG
  
```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993
  
```

```

Sequence 2      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching     : 54.32 [%]
Weight      : 12
  
```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
   ** ** **          *** * * * * ** * * * *
1 : AT-GCCGT-- ----- CGG-AGATTG TTGAC-AGGA AAAGGAAGTC TCG---TGGA

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGGA AAGAGTACAA CG---AGATT
    ** * * *          ** ** *** * * * * * * * * * *
43 : ACACGAGAT- -----GTAGC TGAGATTCTA AGGCAATGGA GAGAGTACAA TGAGCAGATT

118 : GTTGAAGCTT CGGCTGTAA AGAAGGAG-- -AGAAACCGA AACGCAAAGT TCCTGCGAAA
     * * ** * * * * * * * * * * * * * * * *
97 : GAGGCAGAAT CTTGTATCGA TGGTGGTGGT CAAAATCAA TCCGAAAGCC TCCTCCAAAA

175 : GGGTCAAGA AAGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
     ** **** ** * * * * * * * * * * * * * *
157 : GGTTCGAGGA AGGTTGTAT GAAAGGTAAA GGTGGACCTG AAAACGGGAT TTGTGACTAT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTCCAGA ACCGAAAATA
     ***** ** * * * * * * * * * * * * * *
217 : AGAGGAGTTA GACAGAGGAG ATGGGGTAAA TGGGTTGCTG AGATCCGTGA GCCAGACCGA

295 : GGAAGTAGAC TTTGGCTTGG TACTTTTCCT ACCGCGGAAA AAGCTGCTTC CGCTTATGAT
  
```

Fig. 4-12

```

                                -0010181
277 :  ** **** * ***** ** ***** * * * * ***** * *****
      GGTGCTAGGT TGTGGCTCGG TACTTCTCC AGTTCATATG AAGCTGCATT GGCTTATGAC

355 :  GAAGCGGCTA CCGCTATGTA CGGTTCAATG GCTCGTCTTA A-CTTCCC-- --TCA-----
      ** ***** * ***** ** *** * ** * * * * ***** ***
337 :  GAGGCGGCCA AAGCTATATA TGGTCAGTCT GCCAGACTCA ATCTTCCCGA GATCACAAAT

405 :  ----- -GTCTG----- -----TT GGGTCTG--- AGTTTACTAG TACGTCTAGT
      * *** * * * * * * * * * * * * * * * * * * * * * * *
397 :  CGCTCTTCTT CGACTGCTGC CACTGCCACT GTGTCAGGCT CGGTTACTGC ATTTTCTGAT

439 :  CAATCTGAGG TGTGTACGGT TGAAAATAAG GCGGTTGTTT GTGGTGATGT TTTGTGGAAG
      ***** * * * * * * * * * * * * * * * * * * * * * *
457 :  GAATCTGAAG TTTGTGCACG TGAGGATACA AATGCAAGTT CAGGTTTGG TCAGGTGAAA

499 :  CATGAAGATA CTGATTGTGA ATCTAATCCA TT---TAG-- -TCAG---AT TTTAGA----
      * * * * * * * * * * * * * * * * * * * * * * * *
517 :  CTAGAGGATT GTAGCGATGA ATATGTTCTC TTAGATAGTT CTCAGTGTAT TAAAGAGGAG

546 :  -TGTTA-GAG AAGA-GTCTT GTG----GAA CCAGGCCGGA CAGTTG--CA CGG--TTGGA
      ** * * * * * * * * * * * * * * * * * * * * * *
577 :  CTGAAAGGAA AAGAGGAAGT GAGGGAAGAA CATAACTTGG CTGTTGGTTT TGAATTGGA

595 :  CA----TCAA GATATGAATT CTTGCTGAA TTACGATTGG CTGTTA---G AGTTTGAGC-
      ** * * * * * * * * * * * * * * * * * * * * * *
637 :  CAGGACTCGA -AAAGGGAGA CTT---TGGA TGCTTGGTTG ATGGGAAATG GCAATGAACA

647 :  AGCAGTATTG GGGCCAAGTT TTGCGAGAGA AAGAGAAACC GAAGCAGGAA GAAGAGGAGA
      ** * * * * * * * * * * * * * * * * * * * * * *
693 :  AGAACCATTG GAG-TTTGGT GTGGATGAAA CGTTTGATAT TAATGAGCTA -TTGGGTATA

707 :  TACAGCAACA GCAACAGGAA CAG-CAACAG -CAA--CAGC TGCAACCGGA TTTGCTTACT
      * * * * * * * * * * * * * * * * * * * * * *
751 :  TTAAACGACA ACAATGTGTC TGGTCAAGAG ACAATGCAGT ATCAAGTGGA TAGAC--AC-

763 :  GTTGCAAGATT ACGGTTGGCC TTGGTCTAAT G-ATATTGTA AATGATCAGA CTT-CTTGGG
      ** *** * *** * * * * * * * * * * * * * * * *
808 :  ---CCAAATT TCAGTT----- ---ACCAAAC GCAGTTTCCA AAT--TCTAA CTTGCTCGGG

821 :  ATCCTAATGA GTGCTTTGAT ATTAATGAAC TCCTTGGAGA TTTGAATGAA CCTGGTCCCC.
      * * * * * * * * * * * * * * * * * * * * * *
856 :  AGCCTCA--A CCCTATGGAG ATTGCTCAA- --CCAGGAG- -TTG-ATTAT GGATGTCCTT

881 :  ATCAGAGCCA AGACCAAAAC CACGTA-AAT TCTGGTAGTT ATGATTGCA T--CCGCTTC
      ** * * * * * * * * * * * * * * * * * * * * * *
908 :  AT--GTGC-- AGCCCAAGTA TATGGAGAAC TATGGTATTG ATTTAGACCA TCGCAGGTTT

938 :  ----ATCTCG AGCCACACGA --TGG--TCA CGAG--TTCA ATGGTTTGAG TTCTCTGGA-
      ***** * * * * * * * * * * * * * * * * * *
964 :  AATGATCTTG ACATACAGGA CTTGGATTCTT GGAGGAGACA AAGAT----G TTC-ATGGAT

987 :  -TATTTGA
      ** * *
1019 :  CTACATAA

```

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```

Sequence 1      : DREB2B.nuc
Size           : 993
Matching Position : 1 - 993

```

Fig. 4-13

```

Sequence 2      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

Matching Condition.

Matches         : -1
Mismatch        : 1
Gaps            : 1
*NT+           : 2

Matching        : 43.12 [%]
Weight          : 231

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
*** *          * * * * * * * * * * * * * * * *
1 : ATGTC-----ATC C---ATAGAG C-----CA AAAGTAA-----

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGGA AAGAGTACAA CGAGATTGTT
* * * * * * * * * * * * * * * * * * * * * *
26 : --TGATGGTT ---GGT-GC TAAT-----AAGAA-----ACAA CGA-ACCGTC

121 : GAAGCTTCGG CTGTTAAAGA AGGAGAGAAA CCGAAACGCA AAGTTCCTGC GAAAGGGTCG
* * * * * * * * * * * * * * * * * * * * * *
61 : CAAGCT-----AGT-----TCG

181 : AAGAAAGGTT GTATGAAGGG TAAAGGAGGA CCAGATAATT CTCACTGTAG TTTTAGAGGA
* * * * * * * * * * * * * * * * * * * * * *
73 : AGGAAAGGTT GTATGAGAGG AAAAGGTGGA CCCGATAACG CGTCTTGCAC TTACAAAGGT

241 : GTTAGACAAA GGATTGGGG TAAATGGGTT GCAGAGATTC GAGAACCGAA AATAGGAACT
* * * * * * * * * * * * * * * * * * * * * *
133 : GTTAGACAAC GCACTTGGGG CAAATGGGTC GCTGAGATCC GCGAGCCTAA CCGAGGAGCT

301 : AGACTTTGGC TTGGTACTTT TCCTACCGCG GAAAAAGCTG CTTCCGCTTA TGATGAAGCG
* * * * * * * * * * * * * * * * * * * * * *
193 : CGTCTTTGGC TCGGTACCTT CGACACCTCC CGTGAAGCTG CCTTGGCTTA TGACTCCGCA

361 : GCTACCGCTA TGTACGGTTC ATTGGCTCGT CTTAACTTCC CTCAGTCTGT TGGGTCTGAG
*** * * * * * * * * * * * * * * * * * * * * *
253 : GCTCGTAAGC TCTATGGGCC TGAGGCTCAT CTCAACCTCC CTGAGTC-CT TAAG---AAG

421 : TT-TACTAGT ACGTCTAGTC AATCTGAGGT GTGTACGGTT GAAAAATAAGG CGGTTGTTTG
** *** * * * * * * * * * * * * * * * * *
309 : TTACCCTAAA ACGGC--GTC -GTCTCCGGC GTCCAGACT --ACACCAAG CAGCAACACC

480 : TGGTGATGTT TGTGTGAAGC ATGAAGATAC TGATTGTGAA TCTAATCCAT -TTAGTCAGA
* ** * * * * * * * * * * * * * * * * * * *
364 : GGTGGAAA-- -----AAGC A-GCAG---- CCACTCTGAG TC---GCCGT GTTCATCCAA

539 : TTTTAGATGT TAGAGAAGAG TCTTGTGGAA CCAGGCCGGA CAGTTGCACG GTTGGACATC
* * * * * * * * * * * * * * * * * * * * *
408 : --CGAGATGT CA-----TCATGTGGAA ----GAGTGA CAG-----AG G--AGATATC

599 : AAGATATGAA TTCTTCGCTG AATTACGATT TGCTGTTAGA GTTTGAGCAG CAGTATTGGG
* * * * * * * * * * * * * * * * * * * * *
447 : ATGGGA-GCA T-----ATA AACGTGGATT TGCCGGTAAT GGATG-----ATTCTT--

659 : GCCAAGTTTT GCAGGAGAAA GAGAAACCGA AGCAGGAAGA AGAGGAGATA CAGCAACAGC
*** * * * * * * * * * * * * * * * *
491 : --CAA--TAT G-----GGAAGA-----

```

Fig. 4-14

0010181

```

719 : AACAGGAACA GCAACAGCAA CAGCTGCAAC CGGATTTGCT TACTGTTGCA GATTACGGTT
      **** ***          *** *      *** ** *
504 : ----- -AGCTACAA- ----- ---TGTCG-- --TTA-GGAT

779 : GGCCTTGGTC TAATGATATT GTAAATGATC AGACTTCTTG GGATCCTAAT GAGTGCTTTG
      ** *** * **** * * ** * * * **** * *
524 : TTCCATGGGT TCATGA---A GGAGATAATG ATATTTCTCG G----- ----TTTG

839 : ATATTAATGA ACTCCTTGGA GATTGAATG AACCTGGTCC CCATCAGAGC CAAGACCAAA
      ***          ****      ***      * **
566 : ATA----- ---CTTG-- TATTT----- ---CCGG-- -----

899 : ACCACGTAAA TTCTGGTAGT TATGATTTGC ATCCGCTTCA TCTCGAGCCA CACGATGGTC
      *** * * * *** * ** * **** * ** **
582 : ----- ---TGGCTAT TCTAATTGGG ATTCCTTTCA T-TC---CC- -----C

959 : ACGAGTTCAA TGGTTTGAGT TCTCTGGATA TTGA
      **                               *****
615 : AC----- ----- TTTGA

```

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```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

```

```

Sequence 2      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 49.22 [%]
Weight          : 140

```

```

1 : ATGG---CTG TATATGAACA AACCGGAACC GAGCAGCCGA AGAAAAGGAA ATCTAGGGCT
   **** * * ** *** * ** *** **** ** * * ** **
1 : ATGGAAGG AAGAT-AACG GATCGAAACA GAGC-TCCTC TGCTTCTG-- TTGTA-TCCT

58 : CGAGCAGGTG GTTTAACGGT GGCTGATAGG CTAAGAAGT GGAAAGAGTA CAACGAGATT
     **** * * * ** ** ** *** * * **** *** * *** **
56 : CGAG-AAGAC GAAGAAGAGT GGTGA---G C-----CAGT GGA----- -AGCGACGTT

118 : GTTGAAGCTT CGGCTGTTAA AGAAGGA--- GAGAAACCGA AACGCAAAGT TCCTGCGAAA
      ** * ** * * **** * * * * * ** * ** * ** *
99 : ACAGA--GAT GGGAGG---A AGAAGGATTG GCGAGAGC-- -TCGTAGGT TCAAGCCAAA

175 : GGGTCGAAGA AAGGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
      ** **** * **** * * ** * * **** * * ** * **
151 : GGTTCGAAGA AAGGTTGTAT GAGAGGAAA GGTGGACCAG AGAATCCTGT TTGTCGGTTT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTCGAGA ACC-----
      ***** * **** * * **** * * **** * * **** *
211 : AGAGGTGTTT GACAAAGGAT TTGGGGGAAA TGGGTTGCTG AGATACGTGA ACCAGTGAGT

288 : -----G AAAA---TAG --GAACTA-- -GACTTTGGC TTGGTACTTT TCCTACCGCG
      * *** *** * * ** * **** * * ** * * **** *

```



Fig. 4-15

0010181

```

271 : CACCGTGGTG CAAACTCTAG TCGTAGTAAA CGGCTTTGGC TTGGCACGTT TGCTACTGCA

331 : GAAAAAGCTG CTTCCGCTTA TGATGAAGCG GCTACCGCTA TGTACGGTTC ATTGGCTCGT
      * ***** ** *** ** * * * * * * * * *
331 : GCTGAAGCTG CTTTGGCTTA CGACAGAGCT GCTAGTGCA TGTACGGACC CTATGCCAGG

391 : CTTAACTTCC CTCAGTCTGT TGGGTCTGAG TTTACTAGTA CGTCTAGTCA ATCTGAGGTG
      * ** * * * * * * * * * * * * *
391 : TTAAATTTC CGGAAGAT-T TGGGTGGGGG -----AAGGA -----AG-A A-----

451 : TGTACGGTTG AAAATAAGGC GGTGTTTTGT GGTGATGTTT GTGTGAAGCA TGAAGATACT
      * *** * .**** * * * * * * * * *
429 : -GGACG---- --AGGAGGC GG----- --AAAGTT- -----CG GGAGGCTATT

511 : GATTGTGAAT CTAATCCATT TAGTCAGATT TTAGATGTTA GAGAAGAGTC TTGTGAACC
      * *** ** * * * * * * * * *
461 : GGTG-GAAA CTAA--CA-- AAGCCGG--- -TA-ATG--- -----GCGTG AT-TGAA--

571 : AGGCCGGACA GTTGACCGGT TGGACATCAA GA-TATGAAT TCTTCGCTGA ATTACGATT
      **** * **** ** * * * * * * * *
500 : ---CGGA-- -----AGG TGA--AAA GACTATGTAG TCTAC----A ATGAAGA--C

630 : GCTGTTAGAG TTTGAGCAGC AGTATTGGGG CCAAGTTTTG CAGGAGAAAG AGAAACCGAA
      *** ***** ** ** * * * * *
538 : GCT----- ATTGAGC--- ----TT--GG CCA-----TG -ACAAGACTC AGAATCCTAT

690 : GCAGGAAGAA GAGGAGATAC AGCAACAGCA ACAGGAACAG CAACAGCAAC AGCTGCAACC
      * **** * ** * * * * *
576 : G----- --ACTGATAA TGAAATAG-- ---TGAAC-- --CCAGCA-- --GTGAATC

750 : GGATTGCTT ACTGTTGCAG ATTACGGTTG GCCTTGGTCT AATGATATTG TAAATGATCA
      ** * ** * * * *
612 : AGA----- --GGAAG GTTACAG-- -----CT -----ATGATC-

810 : GACTTCTTGG GATCCTAATG AGTGCTTTGA TATTAATGAA CTCCTTGGAG ATTTGAATGA
      *** * ** * * * *
635 : ----- GATTCAAA-- ----TTGGA T-----AA CGGATTGTTG --TATAATGA

870 : ACCTGGTCCC CATCAGAGCC AAGACCAAAA CCACGTAAAT TCTGGTAGTT ATGATTGCA
      **** * * * * *
669 : ACCT----- --CAAA- ----- --GC-

930 : TCCGCTTCAT CTCGAGCCAC ACGATGGTCA CGAGTTCAAT GGTGAGTT CTCTGGATAT
      *** ** * * * * * * * * *
679 : TCCAGTT-AT CACCAGGGA- --GGTGGATT CGA-TTC-AT ATTTGAGTA TTTCAGAT-T

990 : TTGA
      *
732 : CTAG
  
```

+++++

Sequence 1 : DREB2B.nuc  
Size : 993  
Matching Position : 1 - 993

Sequence 2 : DREB2F.nuc  
Size : 834  
Matching Position : 1 - 834

Matching Condition.

Fig. 4-16

0010181

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
*NT         : 2

Matching     : 48.46 [%]
Weight       : 138

```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
   ****                               *** **   ***   ***
1 : ATGG-----AGAA--TCATC-----CTC--

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGA AAGAGTACAA CGAGATTGTT
    * * ***   ****
18 : -----A ATGAA-----ACAA-----

121 : GAAGCTTCGG CTGTTAAAGA AGGAGAGAAA CCGAAACGCA AAGTTCCTGC GAAAGGGTCG
    **   ** **   * * * * * * * * * *
28 : -----TG-----GA AG-----A AGGGTCCTGC-----TCG

181 : AAGAAAGGTT GTATGAAGGG TAAAGGAGGA CCAGATAATT CTCACTGTAG TTTTAGAGGA
    *** * * * * * * * * * * * * * * * *
48 : -----GGG TAAAGGCGGT CCACAAAACG CTCTTTGTCA GTACCGTGGA

241 : GTTAGACAAA GGATTGGGG TAAATGGGTT GCAGAGATTC GAGAACCGAA -AATAGGAAC
    ** ** * * * * * * * * * * * * * * * *
91 : GTCAGGCAAA GGAATTGGGG CAAATGGGTG GCTGAGATCA GAGAGCCCAA GAAGAGG-GC

300 : TAGACTTTGG CTGGTACTT TTCCTACCGC GGAAAAAGCT GCTTCGCTT ATGATGAAGC
    * * * * * * * * * * * * * * * * * *
150 : AAGACTTTGG CTGGCTCTT TCGCTACAGC TGAAGAAGCA GCTATGGCTT ATGATGAGGC

360 : GGCTACCGCT ATGTACGGTT CATTGGCTCG TCTTAACCTC CCTCAGTCTG TTGGGTCTGA
    **   * * * * * * * * * * * * * * * *
210 : TGCCTTGAAG CTCTATGGGC ACGACGCATA CCTCAACTTA CCTCA-TCTT CAGCG-----

420 : GTTACTAGT ACGTCT---A GTCAATCT-- GAGGTGTGTA CGGTTGAAAA TAAGGCGGTT
    * * * * * * * * * * * * * * * * * *
264 : GAATACAAGA CTTTCTCTGA GTAACCTCTA GAGGTTCAAA TGGGT-ACCT TCA--AGGAA

475 : GTTGTGGTG ATGTTGTGT GAAGCATGAA G-ATACTGAT TGTGAAT-CT AATCCATTTA
    **** *   ** * * * *   ****   * * * *   * * * *   * *
321 : GTTTAT---- ATCTATGTTT CCTTCATGTG GTATGCTAAA CGTGAATGCT CAGCC---TA

533 : GTCAGATTTT AGATGTTAGA GAAGAGTCTT GTGGAAC-CA GG----CCGG ACAGTT---G
    **   ** * * * * * * * * * * * * * * * *
374 : GT----GTTT ACATAATCCA GCAAAGACTA GAAGAACTCA AGAAACTGG ACTTTTATCT

585 : CACGGTTGGA CATCAAGATA TGAATTCTTC GCTGAATTAC GATTGCTGT TAGAGT--TT
    **   *   * * * * * * * * * * * * * * * *
430 : CAATCCTATT CTTCTAGTTC T---TCCTCC ACCGAATCAA AACTAATAC TAGCTTTCTT

643 : GAGCAGCAGT ATTGGGGCCA AGTTTTCAG GAGAAAGAGA AACCGAAGCA GGAAGAAGAG
    ** ** ** *   * * * *   * * * * * * * * * *
487 : GATGAGAAG- ACCAG---CA AG-----G GAGAAACAGA CA-ATATGTT CGAAG--GTG

703 : GAGATACAGC AACAGCAACA G---GAACAG CAACAGCAAC AGCTGCAACC GGATTGCTT
    * * * * * * * * * * * * * * * * * *
533 : GTGAT-CAGA AGAAACCAGA GATCGACCTG ACCGAGTTTC TTCAGCAACT AGGAATCTTG

```

Fig. 4-17

0010181

```

760 : ACTGTTGCAG ATTACGGTTG GCCTTGGTCT AATGATATTG TAAATGATCA GACTTCTTGG
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
592 : AAGGATGAAA ATGAAG---- --CAGAACCA AGTGAGGTAG CAGAGTGTCA TTCCCTCCA

820 : GATCCTAATG AGTGCTTTGA TATTAATGAA CTCCTTGGAG ATTTG---AA TGAACCTGG-
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
646 : CCATGGAACG AGCAAGAAGA AACT--GGAA GTCCTTTCAG AACTGAGAAT TTCAGCTGGG

876 : -TCCCC--AT C-AGA-GCCA AG-ACCAAAA CCACGTAAAT TCTGGTAGTT ATGATTGCA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
704 : ATACCCTGAT CGAGATGCCA AGAAGTGAAG CCAC---AAC TATGCAA--T TTGA-CTCCA

930 : TCCGCTTC-- -ATCT-CGAG CCACACGATG --GT---CAC GAGTTCAATG GTTTGAGTTC
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
758 : GCAACTTCGG AAGCTATGAT TTTGAGGATG ATGTATCCTT CCCTTCCAT- CTGGGACTAC

981 : TCTGGA---- TA-TTTGA
      * * * * * * * * * *
817 : TACGGAAGCT TAGATTGA
  
```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+               : 2

Matching          : 48.32 [%]
Weight            : 163
  
```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCG-
    **** * * * * * * * * * * * * * * * * * * * * * * * * * * *
1 : ATGGAAGAAG AGCAAC-CTC CGG--CCAAG AAACGAAACA TGGGGAGATC TAGAAAAGGT

60 : AGCAGGTGGT TTAACGGTGG --CTGATA-- GGCTAAAGAA -----GTGG AAAGAGTACA
    *** * * * * * * * * * * * * * * * * * * * * * * * * * * *
58 : TGCATGAAAG GTAAAGGCGG TCCAGAGAAC GCCACGTGTA CTTTCCGTGG AGTTAG-GCA

110 : ACGAGATTGT TGAAGCTTCG GCTGTTAAAG A-AGGAGAGA AACCGAAACG CAAAGTTCCT
    *** *** * * * * * * * * * * * * * * * * * * * * * * * *
117 : ACGGACTTGG GGTAAAT--G GGTGGCTGAG ATCCGTGAG- --CCTAACCG --TGGGACTC

169 : GCGAAAGGGT CGAAGAAAGG TTGTATGAAG GGTAAAGGAG GACCAGATAA TTCTCACTGT
    * * * * * * * * * * * * * * * * * * * * * * * * * * *
170 : GTCTCTGGCT CG--GCACGT TTAATACCTC GGT---CGAG GCCGCCATGG CTTACGATGA

229 : AG--TTTTAG AGGAGTTA-- GACAAAGGAT TTGGGGTAAA TGGGTTCGAG AGA-TTCGAG
    ** * * * * * * * * * * * * * * * * * * * * * * * *
225 : AGCCGCTAAG AACTCTATG GACACGAGGC TAAACTCAAC TTGG-TGCAC CCACAACAAC

284 : AACCGAAAAT AGGAACTAGA CTTTGGCTTG GTACTTTTCC TACCGCGGAA AAAGCTGCTT
    *** ** * * * * * * * * * * * * * * * * * * * * * * *
284 : AACACAAGT A-GTAGTGAA CAGAAACTT- GTCTTTTCTT GGCCACGG-G TCGGTTCTT
  
```

Fig. 4-18

0010181

```

344 : CCGCTTATGA TGAAGCGGCT ACCGCTATGT ACGGTTTCATT GGCTCG-TCT TAACCTCCCT
      ***** * * * * * * * * * * * * * * * * * * * * * *
341 : GGGCTTATAA T-AAGAAGCT --CGATAT-- --GGTTCATG GGTGGACCT TGGTCTCGGC

403 : CAGTC-TGTT GGGTCTGAGT TTAAGTAGTAC GTCTAGTCAA TCTGAGGTGT GTACGGTTGA
      *** * * * * * * * * * * * * * * * * * * * * * *
394 : CAGGCAAGTT GTTCACGAGG TT-CTTGCTC AGAGAG---A TC-GAGTTTT CTAC--AAGA

462 : AAATAAGGCG GTTGTGTTGTG GT-GATGTTT GT-GTGAAGC ATGAAGATAC --TGATTGTG
      * * * * * * * * * * * * * * * * * * * * * * *
447 : AGATGATGAT CATAGTCATA ATCGATGTTG GTCTTCAAGT GGTTCGAATC TTTGTTGGTT

518 : A--ATCTAAT C-CATTTAGT CAGATTTTGTG ATGTTAGAGA AGAGTCTTG- TGGAACCAGG
      * * * * * * * * * * * * * * * * * * * * * * *
507 : ATTACCTAAA CAAAGTGATT CACA----AG AT-CAAGAGA CCGTTAATGC TACGACTAGT

574 : CCGGACAGTT GCA--CGGTT GGACATCAAG ATATGAATTC TTCGCTGAAT T-----
      * * * * * * * * * * * * * * * * * * * * * * *
562 : TATGGC-GGT GAAGGCGGTG GTGGCTCTAC GT-TAACGTT TTCGACCAAT TTGAAACCAA

623 : ACGATTTGCT G-----T TAGAGTTTGA GCAGCAGTAT TGGGGCCAAG TTT-TGCAGG
      * * * * * * * * * * * * * * * * * * * * * * *
620 : AGAATTTGAT GAGTCAGAAT TATGGATTAT ACAATGGAGC TTGGTCTAGG TTTCTTGTGG

674 : AGAAAGAGAA ACCGAAGCAG GAAGAAGAGG AGATACAGCA ACAGCAACAG GAACAGC-AA
      * * * * * * * * * * * * * * * * * * * * * * *
680 : GGCAAGA-AA A--GAAGACG GAACATGACG TG-----TCA TCGTCGTGTG GATCGTCGGA

733 : CAGCAACAGC TGCAACCGGA TTTGCTTACT GTTGACAGT ACGGTTGGCC TTGGTCTAAT
      ** *** * * * * * * * * * * * * * * * * * * *
732 : CAACAAGGAG AGTATGTTG- GTTCCTAGT GCGGCGGAGA GAGGAT-GCA TAGGCC----

793 : GATATTGTAA ATGATCAGAC TTCTTGGGAT CCTAATGAGT GCTTTGATAT TAATGAACTC
      * * * * * * * * * * * * * * * * * * * * * * *
786 : GGAGTTGGAA --GAGCGAAC -----AGGAT ----AT---- --TTGGAAT GGATGATCT-

853 : CTTGGAGATT TGAATGAACC TGGTCCCAT CAGAGCCAAG ACCAAAACCA CGTAAATCT
      ***** * * * * * * * * * * * * * * * * * *
828 : TTTGGAGATT --GATGATT AGGT-----T TGTG--ATT GGCAAAA--A TGGAGATT--

913 : GGTAGTTATG ATTTGCATCC GCTTCATCTC GAGCCACAGC ATGGTCACGA GTTCAATGGT
      * * * * * * * * * * * * * * * * * * * * * *
875 : -----TCAAG AATTG----- ----GTGTT GTG----AAG A--GTTTCAA CATCCATGGA

973 : TTGAGTTCTC TGGATATTTG A
      * * * * * * * * *
914 : ATTGGTTC-- -----TG A

```

+++++

```

Sequence 1      : DREB2B.nuc
Size            : 993
Matching Position : 1 - 993

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

Matches : -1

Fig. 4-19

0010181

```

Mismatches      :      1
Gaps            :      1
*N+             :      2

Matching        :    39.24 [%]
Weight          :    295

```

```

1 : ATGGCTGTAT ATGAACAAAC CGGAACCGAG CAGCCGAAGA AAAGGAAATC TAGGGCTCGA
   **                                     *** * ** * * ** * * * * **
1 : AT----- --GCCCAGGA AACGGAAGTC TCG---TGGA

61 : GCAGGTGGTT TAACGGTGGC TGATAGGCTA AAGAAGTGA AAGAGTACAA CG---AGATT
   * * * * * ** ** * * * * * * * * * * * * * * * * * * * *
28 : ACACGAGAT- ----GTAGC TGAGATTCTA AGGAAATGGA GAGAGTACAA TGAGCAGACC

118 : GTTGAAGCTT C-GGC--TGT TAAAGAAGGA GAGAAACCGA AACGCAAAGT TCCTGCGAAA
   * * * * * * * * * * * * * * * * * * * * * * * * * *
82 : GAGGCAGATT CTGTCATCGA TGGTGGTGGT TCAAAACCAA TCCGAAAGGC TCCTCCAAAA

175 : GGGTCGAAGA AAGGTTGTAT GAAGGGTAAA GGAGGACCAG ATAATTCTCA CTGTAGTTTT
   * * * * * * * * * * * * * * * * * * * * * * * * * *
142 : CGTTCGAGGA AGGTTGTAT GAAAGGTAAA GGTGGACCTG AAAATGGGAT TTGTGACTAT

235 : AGAGGAGTTA GACAAAGGAT TTGGGGTAAA TGGGTTGCAG AGATTGCGA ACCGAAAATA
   * * * * * * * * * * * * * * * * * * * * * * * * * *
202 : ACAGGAGTTA GACAGAGGAC ATGGGGTAAA TGGGTTGCTG AGATCCGTGA GCCAGGCCGA

295 : GGAAGTAGAC TTTGGCTTGG TACTTTTCTT ACCGCGGAAA AAGCTGCTTC CGCTTATGAT
   ** *** * * * * * * * * * * * * * * * * * * * * * *
262 : GGTGCTAAGT TATGGCTCGG TACTTTCTCT AGTTCATATG AAGCTGCATT GGCTTATGAT

355 : GAAGCGGCTA CCGCTATGTA CGGTTCAATTG GCTCGTCTTA ACTTCCCTCA GTCTGTTGGG
   ** ** * * * * * * * * * * * * * * * * * * * * * *
322 : GAGGCTTCCA AAGCTATTTA CGG----- --TCA GTCTG-----

415 : TCTGAGTTTA CTAGTACGTC TAGTCAATCT GAGGTGTGTA CGGTTGAAAA TAAGGCGGTT
   * * * * * * * * * * * * * * * * * * * * * *
353 : -----CCC GACTCAATCT -----TC C-----

475 : GTTTGTGGTG ATGTTTGTGT GAAGCATGAA GATACTGATT GTGAATCTAA TCCATTTAGT
   * * * * * * * * * * * * * * * * * * * * * *
369 : -----ACTG-----CT-- GCCACTGTGT

535 : CAGATTTTAG ATGTTAGAGA AGAGTCTTGT GGAACCAGGC CGGACAGTTG CACGGTTGGA
   *** * * * * * * * * * * * * * * * * * * * * *
385 : CAG-----G CTCGGTT--A

595 : CATCAAGATA TGAATTCCTC GCTGAATTAC GATTGCTGT TAGAGTTTGA GCAGCAGTAT
   * * * * * * * * * * * * * * * * * * * * * *
397 : C-----TGCATTTTCT GATGAAT---CTG--AAGTTTG-----

655 : TGGGGCCAAG TTTTGCAGGA GAAAGAGAAA CCGAAGCAGG AAGAAGAGGA GATACAGCAA
   * * * * * * * * * * * * * * * * * * * * * *
425 : -----TGCACGT GA-----G GATACA-----

715 : CAGCAACAGG AACAGCAACA GCAACAGCTG CAACCGGATT TGCTTACTGT TGCAGATTAC
   * * * * * * * * * * * * * * * * * * * * * *
441 : -----AA---TG CAA---GAT---CT-----

775 : GGTGGCCCTT GGTCTAATGA TATTGTAAAT GATCAGACTT CTTGGGATCC TAATGAGTGC

```

Fig. 4-20

0010181

```

453 : **** ** **          ***** * ** * *** *
      GGT-----TT GG----- --TCAGA--T CT-----C TAA-----C

835 : TTTGATATTA ATGAACCTCT TGGAGATTG AATGAACCTG GTCCCCATCA GAGCCAAGAC
      **          ***      ****
474 : TT----- --CTC-- --GCATT-- -----C

895 : CAAAACCACG TAAATTCTGG TAGTTATGAT TTGCATCCGC TTCATCTCGA GCCACACGAT
      *****          **** * * ** * * ***
486 : CAAAA----- --TGTTAAG-- --TCCAATAAC TGCAT-----T

955 : GGTCAAGAGT TCAATGGTTT GAGTTCTCTG GATATTTGA
      *** * ***      *** * **      ** *
513 : GGTTA--AGT ----TGG--G GCGT----- --TACTAG-
  
```

+++++

```

Sequence 1      : DREB2C.nuc
Size            : 1026
Matching Position : 1 - 1026
  
```

```

Sequence 2      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621
  
```

Matching Condition.

```

Matches      : -1
Mismatch     : 1
Gaps         : 1
*N+          : 2

Matching      : 43.40 [%]
Weight       : 252
  
```

```

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
   *** * **
1 : ATGTCATC----- --CA----- --TAG-----

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
     ** * *      * * ** ****
14 : -----AGCC A-----AAA GT--AATG-- ----- --ATGTTGGT

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAA-AAGGT TCGAGGAAGG GTTGTATGAA
     * * * * ** *** ** ** * * **** ** ***** * *****
37 : GCTAAT-AAG AAACAA--CG AA----CCGT CCAAGCTAGT TCGAGGAAAG GTTGTATGAG

180 : AGGTAAAGGT GGACCTGAAA ACGGGATTG TGAATATAGA GGAGTTAGAC AGAGGAGATG
     *** ***** ** * *** * **      ** * * ** ***** * * * **
90 : AGGAAAAGGT GGACCCGATA ACGCGTCTTG CACTTACAAA GGTGTTAGAC AACGCACTTG

240 : GGGTAAATGG GTTGCTGAGA TCCGTGAGCC AGACGGAGGT GCTAGTTGT GGCTCGGTAC
     *** ***** ** ***** **** ***** ** ***** ** * * * *****
150 : GGGCAAATGG GTCGCTGAGA TCCGCGAGCC TAACCGAGGA GCTCGTCTT GGCTCGGTAC

300 : TTTCTCCAGT TCATATGAAG CTGCATTGGC TTATGACGAG GCGG--CCAA AGCTATATAT
     *** ** ** ***** ***** ***** ** * * * *****
210 : CTTGACACCC TCCCGTGAAG CTGCTTGGC TTATGACTCC GCAGCTCGTA AGCTCTATGG

358 : G-GTCAGTCT GCCAGACTCA ATCTTCCCGA GATCACAAAT CGCTCTTCTT CGACTGCTGC
     * * ** ** ** ***** * ** ** * * * * * * * * *
  
```

Fig. 4-21

0010181

```

270 : GCCTGAGGCT --CA-TCTCA ACCTCCCTGA G-----TCCTT AAGAAGTTAC
417 : CACTGCCACT GTGTCAGGCT CGGTTACTGC ATTTTCTGAT GAATCTGAAG TTTGTGCACG
    * ** ** * *** * ** * **
313 : C-CTAAACG GCGTC-GTCT C----CGGC -----GTCC---
477 : TGAGGATACA AATGCAAGTT CAGGTTTTGG TCAGGTGAAA CTAGAGGATT GTAGCGATGA
    ** **** ** * ** * ** * ** *
340 : -CAGACTACA ---CCAAG-- CAG---CAAC ACCGGTGGAA --AAAGCA-- GCAGCGA---
537 : ATATGTTCTC TTAGATAGTT CTCAGTGTAT TAAAGAGGAG CTGAAAGGAA AAGAGGAAGT
    *** * ** * * * ** * * *
384 : -----CTC TGAG-----T CGCCGTG--T TCA-----TCCAACGA- ----GATGT
597 : GAGGGAAGAA CATAACTTGG CTGTTGGTTT TGGAATTGGA CAGGACTCGA AAAGGGAGAC
    *** * * * **** * ** *
416 : -----CATCA-----TG TGGA-----GAGT-GA CAGAGGAGA-
657 : TTTGGATGCT TGGTTGATGG GAAATGGCAA TGAACAAGAA CCATTGGAGT TTGGTGTGGA
    * **** ** * * * ** *
443 : -----TATCATGG GA-----GCATATAAA C-----GTGGA
717 : TGAACGTTT GATATTAATG AGCTATTGGG TATATTAAC GACAACAATG TGTCTGGTCA
    *** * ***** *** **
468 : -----TTT GCCGGTAATG -----GATG ATTCT--TCA
777 : AGAGACAATG CAGTATCAAG TGATAGACA CCCAAATTTC AGTTACCAAA CGCAGTTTCC
    * ** *** ** * ** * **
493 : A-----TA-----TGGAAGAAG CTACAATGTC -GTTA-----GGA-TTTCC
837 : AAATTCTAAC TTGCTCGGGA GCCTCAACCC TATGGAGATT GCTCAACCAG GAGTTGATTA
    ** * ** *** * ** ** *** *
528 : --ATGGGTTT ATG--AAGGA G-----A TAATGATATT TCTC-----GGTTTGATAC
897 : TGGATGTCCT TATGTGCAGC CCAAGTATAT GGAGAACTAT GGTATTGATT TAGACCATCG
    * ** *** * ** *** **** * **
570 : T--TG-----TATTT-----CCGGTG-----GCTAT TCTA--ATT GGA-----
957 : CAGGTTCAAT GATCTTGACA TACAGGACTT GGATTTTGA GGAGACAAAG ATGTTTCATGG
    *** *** ** * *
600 : ----TTC---CTT-TCA TTCCCACTT -----
1017 : ATCTACATAA
    *
619 : -----TGA

```

+++++

Sequence 1 : DREB2C.nuc  
 Size : 1026  
 Matching Position : 1 - 1026

Sequence 2 : DREB2E.nuc  
 Size : 735  
 Matching Position : 1 - 735

Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2

Fig. 4-22

Matching : 47.50 [%]  
Weight : 184

0010181

```

1 : ATGCCGTCGG -AGATTGTTG ACAGGAAAAG GAAGTCTCGT GGAACACGAG ATGTAGCTGA
   *** ** **** * * * * * ** *** * * **** *
1 : ATGGAAAAGG AAGATAACGG ATCGAAACAG --AG-CTCCT -CTGCTTCTG TTGTATCCTC

60 : GATTCTAAGG CAATGGAGAG AGTACAATGA GCAGATTGAG GCAGAATCTT GTATCGATGG
   ** *** * * * **** * *** ** * ** * ** * ****
57 : GA---GAAGA CGAAGAAGAG TG---GTTGA GCCAGTGGAA GC--GACGTT ACAGAGATG-

120 : TGGTGGTCCA A--AAT---- -CAATCCGAA AGCCTCCTCC AAAAGGTTTCG AGGAAGGGTT
   ** ** * * * * * * ** * * ** * **** * ** * ****
108 : -GGAGGAAGA AGGATTGGCG AGAGCTCGTA GGGTTCAAGC CAAAGGTTTCG AAGAAAGGTT

173 : GTATGAAAGG TAAAGGTGGA CCTGAAAACG GGATTTGTGA CTATAGAGGA GTTAGACAGA
   ***** ** **** * * * * * **** * **** * **** *
167 : GTATGAGAGG AAAAGGTGGA CCAGAGAATC CTGTTTGTGC GTTTAGAGGT GTTCGACAAA

233 : GGAGATGGGG TAAATGGGTT GCTGAGATCC GTGAGCCAGA CGGAGGTGCT AGGTTGTGGC
   ** ***** **** * **** * **** * **** *
227 : GGGTTTGGGG GAAATGGGTT GCTGAGATAC GTGAACCAG- -TGAGTCAC- -----C

293 : TCGGTACTTT CTCCAGTTCA TATGAAGCTG CATTGGCTTA TGACGAGGCG GCCAAAGCTA
   *** * **** * * * * * * * * * * * * * *
275 : GTGGTGCAAA CTCTAG-TCG TAGTAAACGG CTTTGGCTT- -----G GC-----A

353 : TATATGGTCA GTCTGCCAGA CTCAATCTTC CCGAGATCAC AAATCGCTCT TCTTCGACTG
   * * * * **** * * * * * * * * * * * * *
317 : CGTTTGCT-- -ACTG-CAG- CTGAAGCTGC ----- -TTTGGCT-- -TACGACAG

413 : CTGCCACTGC CACTGTGTCA GGCTCGGTTA CTGCATTTTC TGATGAATCT GAAGTTTGTG
   **** * **** * * * * * * * * * * * * *
357 : ----AGCTGC TA--GTGTCA TGTACGG--A C--CCTATGC ----CAGGT TAAATTT--

473 : CACGTGAGGA TACAAATGCA AGTTCAGGTT TTGGTCAGGT GAAACTAGAG GATTGTAGCG
   * * * * * * * * * * * * * * * * *
399 : CCCG-GAAGA -----T TTG----GGT G-----GGG GA----AG-G

533 : ATGAATATGT TCTCTTAGAT AGTTCTCAGT GTATTAAAGA GGAGCTGAAA GGAAAAGAGG
   * *** * * * * * * * * * * * *
424 : AAGAA----- -GGACGA GGAGGCG----- -GA

593 : AAGTGAGGGA AGAACATAAC TTGGCTGTTG GTTTTGAAT TGGACAGGAC TCGAAAAGGG
   **** **** * * * * * * * * * * *
444 : AAGTTCGGGA ----- -GGCTATTG G--TTGGA- -----AC T---AACAA

653 : AGACTTTGGA TGCTTGGTTG ATGGGAAATG GCAATGAACA AGAACCATTG GAGTTTGGTG
   ** * * * * * * * * * * * * * * *
477 : AGCCGGTAAT GCGGTGATTG AAACGGAA-G G---TGGAAG AGA--CTATG TAGTCT----

713 : TGGATGAAAC GTTTGATATT AATGAGCTAT TGGGTATATT AAACGACAAC AATGTGTCTG
   ***** ** * * **** * *** ** ***** * * *
527 : ACAATGAA-- ----GACGCT ATTGAGC--T TGGCCAT--- ----GACAAG ACTCAGAATC

773 : GTCAAGA--G ACAATGCAGT ATCAAGTGA TAGACACCCA AATTTCAGTT ACCAAACGCA
   * * * * * * * * * * * * * * *
572 : CT-ATGACTG ATAATGAA-- AT--AGTG-- ----AACCCA GCAGT--GAA ATCAGAGGAA

```



Fig. 4-23

```

                                -0010181
831 : GTTTCCAAAT TCTAACTTGC TCGGGAGCCT CAACCCTATG GAGATTGCTC AACCAGGAGT
    * ** *      *** ** ***                ** * **** *** **
619 : GGTACAAA--- GCTA---TGA TCG----- ----ATT CAAATTGGAT AACGGATTGT

891 : TG-ATTATGG ATGTCCTTAT GTGCAGC-CC AGTGATATGG AGAACTATGG TATTGATTGA
    ** ** *** *   *** *      *** ** *** ***      ** * ** ** **
659 : TGTATAATGA A---CCTCA- ---AAGCTCC AGT--TAT-- --CACCAGGG AGGTGGATTG

949 : GACCATCGCA GGTTCATGA TCTTGACATA CAGGACTTGG ATTTTGGAGG AGACAAAGAT
    **          **** * * ****          * ****          ****
706 : GA----- --TTCA--TA TTTTGA----- ----GT ATTT----- ----CAGAT

1009 : GTTCATGGAT CTACATAA
        * * **
731 : -----T C---TAG

+++++

Sequence 1      : DREB2C.nuc
Size           : 1026
Matching Position : 1 - 1026

Sequence 2      : DREB2F.nuc
Size           : 834
Matching Position : 1 - 834

Matching Condition.

Matches      : -1
Mismatches   : 1
Gaps         : 1
* N+         : 2

Matching      : 48.77 [%]
Weight       : 150

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
    ** ** *** ** **
1 : AT-----GG AGA----- AA---TC-----

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
    ** ** * **** *      ***** ** ****
12 : ATCCT---C AATGAA--- --ACAAT--- ----GG AAGAA-----

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAAAAGGTT CGAGGAAGGG TTGTATGAAA
    ***          *** ** *
36 : --GGGT--- ----CCTGCT C-----GG -----

181 : GGTAAGAGTG GACCTGAAAA CGGGATTGTG GACTATAGAG GAGTTAGACA GAGGAGATGG
    ***** * * ** **** ** ***** * ** * * **** ** ** **** **
49 : GGTAAGAGCG GTCCACAAAA CGCTCTTTGT CAGTACCGTG GAGTCAGGCA AAGGACTTGG

241 : GGTAATAGGG TTGCTGAGAT CCGTGAGCC- -AGACGGAGG TGCTAGGTTG TGGCTCGGTA
    ** ***** * ***** * * ***** *** **** ** ** * ***** **
109 : GGCAATAGGG TGGCTGAGAT CAGAGAGCCC AAGA-AGAGG -GCAAGACTT TGGCTTGGCT

299 : CTTTCTCCAG TTCATATGAA GCTGCATTGG CTTATGACGA GGCGGCCAAA GCTATATATG
    ***** * * * *** ** ** ***** ** ** ***** * ****
167 : CTTTCGCTAC AGCTGAAGAA GCAGCTATGG CTTATGATGA GGCTGCCTTG AAACCTCTATG

359 : GTCAGTCTGC CAGACTCAAT CTTCCCGAGA TCACAAATCG CTCTTCTTC- GACTGCTGCC
    * ** **      ***** *** ** ***          ***** * ** *
227 : GGCACGAGCG ATACCTCAA- CTTACC----- TCA----- -TCTTCAGCG GAATAC-AAG

```

Fig. 4-24

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```

418 : ACTGCCACTG TGTGAGGCTC GGTTACTGCA TTTTCTGATG AATCTGAAGT TTGTGCACGT
    ** * *** ** * *** *      *   *** *** * * * * *
273 : ACCTTCTCTG AGTAACTCTC AG-----A GGTTCAAATG GGT---ACCT TCAAGGAAGT

478 : GAGGATACAA ATG-CAAGTT CAGGTTTTGG TCAGGTGAAA CTAGAGGATT GT-AGCGATG
    ***   ***   ** ** * *** * * * *** * * * * *
323 : --TTATATCT ATGTTTCCTT CA---TGTGG T-ATGCTAAA C--GTGAATG CTCAGCCTAG

536 : AATATGTTCT CTTAGATAGT TCTCAGTGTA TTAAGAGGA GCTGAAAGGA AAAGAGGAAG
    ***** * *** *   *** *   *** ** * * * * *
375 : ----TGTC- ---ACATAAT --CCAGCAAA GACTAGAAGA ACTCAA--GA AAATGGACT

596 : TGAGGGAAGA ACATAACTTG GCTGTTGGTT TTGGAATTGG ACAGGACTCG AAAAGGGAGA
    *   *   ** **   ** * *** *   *   ** ** ** * *
423 : T----TTATC TCAATCCTAT TCTTCTAGTT CT--TCCTCC AC-CGAATCA AAAACTAATA

656 : CTTTGGATGC TTGGTTGATG GGA--AATGG CAATG----A ACA-AGAA-C CATTGGAGTT
    **   ** ** * * * * * ** * * * * * * * * *
476 : CT-----AGC TTTCTTGATG AGAAGACCAG CAAGGGAGAA ACAGACAATA TGTTCAAGG

708 : TGGTG--TGG ATGAAACGTT TGATATTAAT GAGCTATTGG GTATATTAAC CGACAACAAT
    ***** * * * * *   *** *   ** *   *   ** * *
531 : TGGTGATCAG AAGAAACCAG AGATCGACCT GACC----GA GTTTCCTT--- CAGCAACTAG

766 : GTGTCTGGTC AAGA-GACAA T---GCAGTA TCAAGTGGAT AGACACCCAA ATTTCAAGTTA
    *   ** *   * * * * * *   **** *   ***** ** * * * *
584 : GAATCTTG-A AGGATGAAAA TGAAGCAGAA CCAAGTG--- AGGTAGCAGA GTGTCA-TTC

822 : CCAAACGCAG TTTCCAAATT CTAAGTTGCT CGGGAGCCTC AACCCATATGG AGATTGCTCA
    **   ----- **** *   *** **   * * *   ** *   *   ** *
639 : CC----- -CTCCACCAT GGAACGAGC- AAGAAG---- AAAGTGAAG TCCTTCAGA

882 : AC-CAGGAGT TGATTATGGA TGTCTTAT- GTGCAGCC-- -CAGTGATAT GGAGAACTAT
    ** ** * * * *   *** *   *** **   * * ***   ***** *   *
685 : ACTGAGAATT TCAGCTGGGA TACCCTGATC GAGATGCCAA GAAGTGA-AA CCACAACCTAT

937 : GGTA-TTGA- TTTAG-ACCA TCGCAGGTTT AATGATCTTG A-CATACAGG A--CTTGGAT
    * * ***** * * * *   *** * *   ***** ** *   *   *
744 : GCAATTTGAC TCCAGCAACT TCGGAAG--C TATGATTTTG AGGATGATGT ATCCTTCCCT

991 : TTTGGAGGAG ACAAAGATGT TCATGGATCT ACATAA
    *   * * * * *   * * *   * * *
802 : TCCATCTGGG ACTACTACG- -GAAGCTTAG A-TTGA

```

+++++

```

Sequence 1      : DREB2G.nuc
Size            : 1026
Matching Position : 1 - 1026

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 48.42 [%]

```

Fig. 4-25

Weight : 130

0010181

```

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACCAGA TGTAGCTGAG
   **          **** * ***          ***
1 : AT----- --GGAA---G AAG----- --AGC-----

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
   * ** *** *   ***   ** **          **          ****
14 : AACCTCCGGC CA-----AGA ----AACGA- ----- --AA----- --CATGG-

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CCAAAAGGTT CGAGGAAGGG TTGTATGAAA
   **          * * * * * * * * * * * * * * * *
41 : ---GG----- ----- --AGAT CTAGAAAAGG TTGCATGAAA

181 : GGTAAGGTG GACCTGAAAA CGGGATTTGT GACTAT-AGA GGAGTTAGAC AGAGGAGATG
   ***** * * * * * * * * * * * * * * * * * * * *
67 : GGTAAGGCG GTCCAGAGAA CGCCACGTGT -ACTTTCCGT GGAGTTAGGC AACGGACTTG

240 : GGGTAAATGG GTTGCTGAGA TCCGTGAGCC AGACGGAGGT GCTAGGTTGT GGCTCGGTAC
   ***** * * * * * * * * * * * * * * * * * * * *
126 : GGGTAAATGG GTGGCTGAGA TCCGTGAGCC TAACCGTGGG ACTCGTCTCT GGCTCGGCAC

300 : TTTCTCCAGT TCATATGAAG CTGCATTGGC TTATGACGAG GCGGCCAAAG CTATATATGG
   ** *   ** * * * * * * * * * * * * * * * * * * *
186 : GTTTAATACC TCGGTCGAGG CCGCCATGGC TTACGATGAA GCCGTAAGA AACTCTATGG

360 : TCAGTCTGCC AGACTCAATC TTCCCGAGAT CACAAATCGC TCTTCTTCCA CTGCTGCCAC
   ** ** * * * * * * * * * * * * * * * * * * * *
246 : ACACGAGGCT AAACCTCAA-C TTGGTGCACC CACAACAACA ACAACAAGTA GTAGTG-AAC

420 : TGCCACTGTG TCAGGCTC-G GTTACTGCAT TTTCTGATGA ATCTGAAGTT TGTGCACGTG
   * * * * * * * * * * * * * * * * * * * * * * *
304 : AGAAACT-TG TCTTTTCTG GCCACGG--- -GTCGGGT-- -TCTGGGCT TAT-AATAAG

479 : AGGATACAAA TGCAAGTTCA GGTTTTGGTC AGGTGAAAC- TAGAGGATTG TAGCGATGAA
   * * * * * * * * * * * * * * * * * * * * * * *
355 : AAGCTCGATA TG---GTTCA TGGGTTGGAC CTTGGTCTCG GCCAGGCAAG T--TGTTTAC

538 : TATGTTCT-- CTTAGATAGT TCTCAGTGTA TTA----AAG AGGA-GCTGA AAGGAAAAGA
   * * * * * * * * * * * * * * * * * * * * * * *
410 : GAGGTTCTTG CTCAGAGAGA TC-GAGTTTT CTACAAGAAG ATGATGATCA TAGTCATAAT

591 : GGAAGTGAG- --GGAAGAAC ATAACCTGGC TGTGGTTTT GGAATTGGAC A---GGAAGT
   ** ** *   ***   *   *   * * * * * * * * * *
469 : CGATGTTCTG CTTCAAGTGG TTCGAATCTT TGTGGTTAT -TACCTAAAC AAAGTGATTC

645 : GAAAAG---G GAGACTTTGG ATGCT----- TGGTTGATG- -GGAATGGC AATGAACAAG
   **          ***** *   ***** * * * * * * * *
528 : ACAAGATCAA GAGACCGTTA ATGCTACGAC TAGTT-ATGG CGGTGAAGGC GGTGGTGGCT

695 : AACCATTGGA GTTT--GGTG TGGATGAAAC GTTTGATATT AATGAG---- --CTATTGGG
   * **   **** *   *****   ** **   *****   *** *
587 : CTACGTTAAC GTTTTCGACC AATTTGAAAC CAAAGAATTT GATGAGTCAG AATTATGGAT

747 : TAT---ATTA AACGACAACA ATGTGTCT-- --GGTCAAG- --AGACAATG CAGTATCAAG
   *** ** * *   * * * * *   ** *****   *** * * * * *
647 : TATACAATGG AGCTTGGTCT AGGTTTCTTG TGGGGCAAGA AAAGAAGACG GAACATGACG

797 : TG-GATAGAC ACCCAAAT-T TCAGTTACCA AACGCAGTTT CCAAATTCTA ACTTGCTCGG

```

Fig. 4-26

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** ** * *      ** ** * * ** *      *** *      *** * **** *
707 : TGTCATCGTC GTGTGGATCG TCGGACAACA AGGAGAGTAT GTTGGTTCCT AGTTGCGGCG

855 : GAGCCTCAAC CCTATGGAGA TTGCTCAACC AGGAGTT-GA TTATGGATGT CCTTATGTGC
***      ***      *** * *      ***** ** * **      *** **
767 : GAG----- ----AGAGG ATGCATAGGC CGGAGTTGGA AGAGCGAACA GGATATTGGA

914 : AGCCCACTGA ---TATGGAG AACTATGGTA TTGATTTAGA CCATCGCAGG TTCAATGATC
*      ***      * ***** *      *** * * * *** *      ** *      *** **
815 : AAATGGATGA TCTTTTGGAG ATTGATGATT TAGGTTT-GT TGATTG---- -GCAAAAATG

971 : TTGACATACA GGAATTGGAT TTTGGAGGAG ACAAAGATGT TCATGGA--T CTACATAA
** * ** ** ***** ** ** *** * * * ***** *      * *
869 : GAGA-TTTCA AGAATTGGTG TTGTGAAGAG TTTCA-ACAT CCATGGAATT GGTTCGTA

+++++

Sequence 1      : DREB2C.nuc
Size           : 1026
Matching Position : 1 - 1026

Sequence 2      : DREB2H.nuc
Size           : 534
Matching Position : 1 - 534

Matching Condition.

Matches        : -1
Mismatch      : 1
Gaps          : 1
*N+           : 2

Matching       : 48.34 [%]
Weight        : 62

1 : ATGCCGTCGG AGATTGTTGA CAGGAAAAGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG
*****
1 : ATGCC----- CAGGAAACGG AAGTCTCGTG GAACACGAGA TGTAGCTGAG

61 : ATTCTAAGGC AATGGAGAGA GTACAATGAG CAGATTGAGG CAGAATCTTG TATCGATGGT
*****
46 : ATTCTAAGGA AATGGAGAGA GTACAATGAG CAGACCGAGG CAGATTCTTG CATCGATGGT

121 : GGTGGTCCAA AATCAATCCG AAAGCCTCCT CAAAAGGTT CGAGGAAGGG TTGTATGAAA
*****
106 : GGTGGTCCAA AACCAATCCG AAAGGCTCCT CAAAACGTT CGAGGAAGGG TTGTATGAAA

181 : GGTAAGGTG GACCTGAAAA CGGGATTTGT GACTATAGAG GAGTTAGACA GAGGAGATGG
*****
166 : GGTAAGGTG GACCTGAAAA TGGGATTTGT GACTATACAG GAGTTAGACA GAGGACATGG

241 : GGTAATGGG TTGCTGAGAT CCGTGAGCCA GACGGAGGTG CTAGGTTGTG GCTCGGTACT
*****
226 : GGTAATGGG TTGCTGAGAT CCGTGAGCCA GGCCGAGGTG CTAAGTTATG GCTCGGTACT

301 : TTCTCCAGTT CATATGAAGC TGCATTGGCT TATGACGAGG CGGCCAAAGC TATATATGGT
*****
286 : TTCTCTAGTT CATATGAAGC TGCATTGGCT TATGATGAGG CTTCCAAAGC TATTTACGGT

361 : CAGTCTGCCA GACTCAATCT TCCCGAGATC ACAAATCGCT CTTCTTCGAC TGCTGCCACT
*****
346 : CAGTCTGCCC GACTCAATCT TCC----- ----AC TG-----CT

```

Fig. 4-27

0010181

```

421 : GCCACTGTGT CAGGCTCGGT TACTGCATTT TCTGATGAAT CTGAAGTTTG TGCACGTGAG
      *****
375 : GCCACTGTGT CAGGCTCGGT TACTGCATTT TCTGATGAAT CTGAAGTTTG TGCACGTGAG

481 : GATACAAATG CAAGTTCAGG TTTTGGTCAG GTGAAACTAG AGGATTGTAG CGATGAATAT
      *****
435 : GATACAAATG CAAGATCTGG TTTTGGTC-- -----

541 : GTTCTCTTAG ATAGTTCTCA GTGTATTAAA GAGGAGCTGA AAGGAAAAGA GGAAGTGAGG
      ** ****
463 : ----- --AGATCTC- -----

601 : GAAGAACATA ACTTGGCTGT TGGTTTTGGA ATTGGACAGG ACTCGAAAAG GGAGACTTTG
      ** ***
470 : -----TA ACT-----

661 : GATGCTTGGT TGATGGGAAA TGGCAATGAA CAAGAACCAT TGGAGTTTGG TGTGGATGAA
475 : -----

721 : ACGTTTGATA TTAATGAGCT ATTGGGTATA TTAACGACA ACAATGTGTC TGGTCAAGAG
      ** *
475 : -----TC T-----

781 : ACAATGCAGT ATCAAGTGGA TAGACACCCA AATTTTCAGTT ACCAAACGCA GTTTCCAAAT
      ****
478 : -----CGCA -TTTCCAA-

841 : TCTAACTTGC TCGGGAGCCT CAACCCATG GAGATTGCTC AACCAGGAGT TGATTATGGA
490 : -----

901 : TGTCTTATG TGCAGCCCAG TGATATGGAG AACTATGGTA TTGATTAGA CCATCGCAGG
      *** * ** *** * **** * * *** **
490 : -----ATG TTAAGTCCA- -----AT AACT---GCA TTGGTTAAG-

961 : TTCAATGATC TTGACATACA GGACTTGGAT TTTGGAGGAG ACAAAGATGT TCATGGATCT
      ****
520 : -----TTGG-----GGCGTT

1021 : ACATAA
      ** **
530 : AC-TAG

```

+++++

```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

```

Fig. 4-28

Matching : 49.93 [%]  
Weight : 81

0010181

```

1 : ATG-----TC ATC--CATAG AG-----CCAAA
   ***          *** * * * *
1 : ATGGAAGAGG AAGATAACGG ATCGAAACAG AGTCCTCTG CTCTGTTGT ATCCTCGAGA

21 : AG-----TAA TGATGGTTG- ----GT---- ----GCTA- ----AT---- --AAGAA---
   **          ** * * * * *          * * * *          * * * *          * * * *
61 : AGACGAAGAA GAGTGGTTGA GCCAGTGGAA GCGACGTTAC AGAGATGGGA GGAAGAAGGA

48 : -----AC AACGAACCGT CCAAGCTA-- -GTTGAGGA AAGGTTGTAT GAGAGGAAAA
   *          * * * * *          * * * * *          * * * * *          * * * * *
121 : TTGGCGAGAG CTCGTAGGT TCAAGCCAAA GTTTCGAAGA AAGGTTGTAT GAGAGGAAAA

97 : GGTGGACCCG ATAACGCGTC TTGCACTTAC AAAGGTGTTA GACAACGCAC TTGGGGCAAA
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
181 : GGTGGACCAG AGAATCCTGT TTGTCGGTTT AGAGGTGTTT GACAAAGGTT TTGGGGGAAA

157 : TGGGTCGCTG AGATCCGCGA GCC-----T AACCGAGGAG C-----TCGT-----
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
241 : TGGGTTGCTG AGATACGTGA ACCAGTGAGT CACCGTGGTG CAAACTCTAG TCCTAGTAAA

196 : ---CTTTGGC TCGGTACCTT CGACACCTCC CGTGAAGCTG CCTTGGCTTA TGACTCCGCA
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
301 : CGGCTTTGGC TTGGCAGTT TGCTACTGCA GCTGAAGCTG CTTTGGCTTA CGACAGAGCT

253 : GCTCGTAAGC TCTATGGGCC TGAGGCTCAT CTCAACCTCC CTGAGTCCTT AAGAAGTTAC
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
361 : GCTAGTGTCA TGTACGGACC CTATGCCAGG TTAAATTTCG CGGAAGATTG GGTGGGGGA

313 : CCTAAACCGG CGTCGTCTCC GCGTCCCG ACTACACCAA GCAGCAACAC CGGTGGAAAA
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
421 : AGGAAGAAG- -GACG----A GGAGCGGAA AGTTCGGGAG GC-----TAT TGGTTG-GAA

373 : AGCAGCAGCG ACTCTGAGTC GCCGTG-TTC ATCC--AACG -AGATGTCAT CATGTGG--A
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
469 : ACTAACAAG CCGGTAA--T GCGGTGATTG AAACGGAAGG TGGAAAAGAC TATGTAGTCT

427 : AGAGTGACAG AGGAGAT--A TCATGGGAGC AT-ATAA-AC GTGGA----T TTG-CCGGTA
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
527 : ACAATGA-AG ACGCTATTGA GCTTGG--CC ATGACAAGAC TCAGAATCCT ATGACTGATA

478 : ATGGA----T G-ATTCTTCA ---ATATGGG AAGAA-GCTA CAATGTCGTT AGGATTTCCT
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
584 : ATGAAATAGT GAACCCAGCA GTGAAATCAG AGGAAGGTTA CAGCTATGAT -CGATTCAAA

529 : TGGGTTTCATG AA--GGAG-A TAATGATATT TCTCGGTTTG ATACTTGTAT TTCCGGTGG-
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
643 : TTGGATAACG GATTGTTGTA TAATGA-ACC TCAAAGCT-- CCAGTTATCA CCAGGGAGGT

585 : CTATTCTAAT TGGGATTCCT TTCATTCCCC ACTTTGA
   * * * * * * * * * *          * * * * *          * * * * *          * * * * *
700 : GGATTC-GAT TCATATTTTG AGTATTTTCA ATTCTAG

```

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Sequence 1 : DREB2D.nuc  
Size : 621  
Matching Position : 1 - 621

Fig. 4-29

0010181

Sequence 2 : DREB2F.nuc  
 Size : 834  
 Matching Position : 1 - 834

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 46.13 [%]  
 Weight : 164

```

1 : ATGTCATCCA TAGAGCCAAA AGTAATGATG GTTGGTGCTA ATAAGAAACA ACGAACCGTC
   ***      *** ** *      * * * * *
1 : ATG----- --GAG--AA A----- --TCATCCTC A-ATGAAACA A-----

61 : CAAGCTAGTT CGAGGAAAGG TTGTATGAGA GGAAAAGGTG GACCCGATAA CGCGTCTTGC
   * ** * * * * * * * * * * * * * * * *
28 : -----T GGAAGAAGGG TCCTGCTCGG GGTAAGGCG GTCCACAAAA CGCTCTTTGT

121 : ACTTACAAAG GTGTTAGACA ACGCACTTGG GGCAAATGGG TCGCTGAGAT CCGCGAGCCT
   *** * * * * * * * * * * * * * * * *
79 : CAGTACCGTG GAGTCAGGCA AAGGACTTGG GGCAAATGGG TGGCTGAGAT CAGAGAGCCC

181 : AA-CCGAGGA GCTCGTCTTT GGCTCGGTAC CTTGACACC TCCCGTGAAG CTGCCTTGGC
   ** **** ** * **** **** ** * **** ** * **** * * *
139 : AAGAAGAGG- GCAAGACTTT GGCTTGGCTC TTTCGCTACA GCTGAAGAAG CAGCTATGGC

240 : TTATGACTCC GCAGCTCGTA AGCTCTATGG GCCTGAGG- ----- --CTCATCT
   ***** ** ** * * ***** ** ** * *****
198 : TTATGATGAG GCTGCCTTGA AACTCTATGG GCACGACGCA TACCTCAACT TACCTCATCT

285 : ----- -CAA---CCT CCCTGAGT-- CTTAAGAAG T----- TACCCTAAA-
   *** * * * * * * * * * * * * * * *
258 : TCAGCGGAAT ACAAGACCTT CTCTGAGTAA CTCTCAGAGG TTCAAATGGG TACCTTCAAG

319 : -----ACG GCGTCGTCTC C-----GG -----C GT-----CCC AGACT-----
   * * * * * * * * * * * * * * * *
318 : GAAGTTTATA TCTATGTTTC CTTCATGTGG TATGCTAAAC GTGAATGCTC AGCCTAGTGT

346 : --ACACCAAG CAGC-AACAC CGGTGGAA-- ----AAAGC- -----
   *** * **** * * * * * * * * *
378 : TCACATAATC CAGCAAAGAC TAGAAGAACT CAAGAAAACCT GGACTTTTAT CTCAATCCTA

376 : -----AG- -----CA GCG----- -ACTCTGAGT CGCCGTGTTT AT-----C
   **      ** **      *** * * ** * * *
438 : TTCTTCTAGT TCTTCCTCCA CCGAATCAAA AACTAATACT AGCTTTCTTG ATGAGAAGAC

405 : CAAC----GA GA---TGTC TAATG-TGGA AG--AGTGA- CAGAGG---- -AGATAT---
   ** * ** ** * * * * * * * * * *
498 : CAGCAAGGGA GAAACAGACA ATATGTTTCA AGGTGGTGAT CAGAAGAAAC CAGAGATCGA

446 : CATG----- --GGAGC A--TA----- --TAAACG-T GGATTTG--- ----CC---
   * **      *** * * * * * * * * *
558 : CCTGACCGAG TTTCTTCAGC AACTAGGAAT CTTGAAGGAT GAAAATGAAG CAGAACCAAG

474 : ---GGTAATG GA---TGATT ---CTTCAAT ATGG----- ---GAAGAAG CTACAATGTC
   **** ** * *** ** * **** ***** ** **
618 : TGAGGTAGCA GAGTGTCAAT CCCCTCCACC ATGGAACGAG CAAGAAGAAA CTGGAA-GTC

```

Fig. 4-30

0010181

```

516 : GTT----- --AGGATTTC -CATGGGTT- -CATGAAGGA GAT----- AATGA-----
      **          ** *****      * * * * * * * * * * * * * * *
677 : CTTTCAGAAC TGAGAATTTC AGCTGGGATA CCCTGATCGA GATGCCAAGA AGTGAAACCA

552 : -TATTTCTCG GTTTGATACT TGTATTTCCG GTGGCTATTC TAATTGGGAT -----TCCT
      * * * * * ***** * * * * * * * * * * * * * * *
737 : CAACTATGCA ATTTGACTCC AGCAACTTCG GAAGCTATGA TTTTGAGGAT GATGTATCCT

605 : TTCATTCC-- -----CCAC T----- --TTGA
      * * * * * * * * * * * * * * *
797 : TCCCTTCCAT CTGGGACTAC TACGGAAGCT TAGATTGA

```

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```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 45.04 [%]
Weight          : 190

```

```

1 : ATGTCATCCA TAGAGCCAAA AGTAATGATG GTTGGTGCTA ATAAGAAACA ACGAACCGTC
   ***          ** ** ** * * * * * * * * * * * * * * *
1 : ATG----- --GA-AGAAG AGCAA----- --CCTCCGG CCAAGA--A ACGAAACAT-

61 : CAAGCTAGTT CGAGGAAAGG TTGTATGAGA GGAAAAGGTG GACCCGATAA CGCGTCTTGC
     * * * * * ***** ** * * * * * * * * * * * * * * *
39 : --GGGGAGAT CTAGAAAAGG TTGCATGAAA GGTAAAGGCG GTCCAGAGAA CGCCACGTGT

121 : ACTTACAAAG GTGTTAGACA ACGCACTTGG GGCAAATGGG TCGCTGAGAT CCGCGAGCCT
     **** * * * * * ***** ** * * * * * * * * * * * * * * *
97 : ACTTTCGGTG GAGTTAGGCA ACGGACTTGG GGTAAATGGG TGGCTGAGAT CCGTGAGCCT

181 : AACCAGGAGG CTCGTCTTTG GCTCGGTACC TTCGACACCT CCCGTGAAGC TGCCTTGGCT
     ***** ** ***** ** ***** ** * * * * * * * * * * *
157 : AACCGTGGGA CTCGTCTCTG GCTCGGCACG TTTAATACCT CGGTGAGGC CGCCATGGCT

241 : TATGACTCCG CAGCTCGTAA GCTCTATGGG CCTGAGGCTC ATCTCAAC-- ----CTCCCT
     ** ** * * * * * ***** * * * * * * * * * * * * * * *
217 : TACGATGAAG CCGCTAAGAA ACTCTATGGA CACGAGGCTA AACTCAACTT GGTGCACCCA

295 : GA-----GTC CTTAAGAAGT --TACCCTAA AAC----- --GGC-- --GTCG--
     * * * * * * * * * * * * * * * * * * * * *
277 : CAACAACAAC AACAAGTAGT AGTGAACAGA AACTTGTCTT TTTCTGGCCA CGGGTCGGGT

328 : TCTCCGGC-- -----G TC-----CCAG
     *** ** * * * * * * * * * * * * * * *
337 : TCTTGGGCTT ATAATAAGAA GCTCGATATG GTTCATGGGT TGGACCTTGG TCTCGGCCAG

343 : AC-----TA CACCAAG--- -----CAGCA ACACCG---G TGGAAAAAGC AGCAGCGACT

```



Fig. 4-31

```

                                0010181
      *   *   *   *   *   *   *   *   *   *   *   *   *
397 :  GCAAGTTGTT CACGAGGTTT TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGATGATGAT

386 :  CTGAGTC--- -GCCGTGTTC ATC--CAA-- ----CGA--- ---GAT-GTC ATCATGTGGA
      *   ****   *   ***** **   ***   ***   *   *   *   *   *
457 :  CATAGTCATA ATCGATGTTC GTCTTCAAGT GGTTCGAATC TTTGTTGGTT ATTACCTAAA

427 :  -AGAGTGA-- CAGAGGA--- -----GA -TA-TCATGG ----GA----
      *   ***** **   *   **   **   *   *   *   *   *
517 :  CAAAGTGATT CACAAGATCA AGAGACCGTT AATGCTACGA CTAGTTATGG CGGTGAAGGC

453 :  -----GC- --ATATAAAC GT----- -----GGATTT GCCG-GT---
      **   *   *   *   *   *   *   *   *   *   *   *   *
577 :  GGTGGTGGCT CTACGTTAAC GTTTTCGACC AATTGAAAC CAAAGAATTT GATGAGTCAG

477 :  -----AATGG -----ATGATTCTT- ----CAATA TGGGAAGAAG
      ***** **   *   *   *   *   *   *   *   *   *   *
637 :  AATTATGGAT TATACAATGG AGCTTGGTCT AGGTTTCTTG TGGGCAAGA AAAGAAGACG

506 :  CTACA----- --AT-GTC GTTAGGAT-- -----TTCC-
      ***   **   *   *   *   *   *   *   *   *   *   *
697 :  GAACATGACG TGTCATCGTC GTGTGGATCG TCGGACAACA AGGAGAGTAT GTTGGTTCTT

528 :  -----ATGGGT TCAT----- --GAAG ---GA---G ATA-----
      **   *   *   *   *   *   *   *   *   *   *   *
757 :  AGTTGCGGCG GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTTGGAA

548 :  ----ATGATA TTTCTCGGTT TGAT-ACTT- -GTATTTCCG GTGGCTA--- -----TTC
      ***** ***   *   *   *   *   *   *   *   *   *   *
817 :  ATGGATGATC TTTTGGAGAT TGATGATTTA GGTGTTGTGA TTGGCAAAA TGGAGATTTT

591 :  --TAATTGG- ----GATTC CTTTCATTCC CCA----- --CTTTGA
      ***** **   *   *   *   *   *   *   *   *   *   *
877 :  AAGAATTGGT GTGTGAAGA GTTCAACAT CCATGGAATT GGTTCGTA

```

+++++

```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 47.49 [%]
Weight            : 113

```

```

1 :  ATG----- TCAT----- CCA---TAG -----AGCCA----
      ***          ** *   * *   ***          ** *
1 :  ATGCCCAAGG AACGGAAGTC TCGTGAACA CGAGATGTAG CTGAGATTCT AAGGAAATGG

19 :  --AAAGT--A ATG----- --ATGG TTGGTGCT-A ATAAGAAACA
      *   *** *   *   *   *   *   *   *   *   *   *
61 :  AGAGAGTACA ATGAGCAGAC CGAGGCAGAT TCTTGCATCG ATGGTGGTGG TTCAAAACCA

```

Fig. 4-31

```

                                0010181
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
397 : GCAAGTTGTT CACGAGGTTT TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGATGATGAT

      *   *   *   *   *   *   *   *   *   *   *   *   *   *
386 : CTGAGTC--- -GCCGTGTTT ATC--CAA-- ----CGA--- ---GAT-GTC ATCATGTGGA
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
457 : CATAGTCATA ATCGATGTTT GTCTTCAAGT GGTTCGAATC TTTGTTGGTT ATTACCTAAA

      *   *   *   *   *   *   *   *   *   *   *   *   *   *
427 : -AGAGTGA-- CAGAGGA--- -----GA -TA-TCATGG ----GA----
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
517 : CAAAGTGATT CACAAGATCA AGAGACCGTT AATGCTACGA CTAGTTATGG CGGTGAAGGC

      *   *   *   *   *   *   *   *   *   *   *   *   *   *
453 : -----GC- --ATATAAAC GT----- -----GGATTT GCCG-GT---
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
577 : GGTGGTGGCT CTACGTTAAC GTTTTCGACC AATTGAAAC CAAAGAATTT GATGAGTCAG

      *   *   *   *   *   *   *   *   *   *   *   *   *   *
477 : -----AATGG -----ATGATTCTT- ----CAATA TGGGAAGAAG
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
637 : AATTATGGAT TATACAATGG AGCTTGGTCT AGGTTTCTTG TGGGCAAGA AAAGAAGACG

      *   *   *   *   *   *   *   *   *   *   *   *   *   *
506 : CTACA----- -AT-GTC GTTAGGAT-- -----TTCC-
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
697 : GAACATGACG TGTCATCGTC GTGTGGATCG TCGGACAACA AGGAGAGTAT GTTGGTTCCT

      *   *   *   *   *   *   *   *   *   *   *   *   *   *
528 : -----ATGGGT TCAT----- -GAAG ---GA---G ATA-----
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
757 : AGTTGCCGCG GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTTGGAA

      *   *   *   *   *   *   *   *   *   *   *   *   *   *
548 : ---ATGATA TTTCTCGGTT TGAT-ACCT- -GTATTTCCG GTGGCTA--- -----TTC
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
817 : ATGGATGATC TTTTGAGAT TGATGATTTA GGTGTTGTTA TTGGCAAAAA TGGAGATTTT

      *   *   *   *   *   *   *   *   *   *   *   *   *   *
591 : --TAATTGG- ----GATTC CTTTCATTCC CCA----- --CTTTGA
      *   *   *   *   *   *   *   *   *   *   *   *   *   *
877 : AAGAATTGGT GTTGTGAAGA GTTTCACAT CCATGGAATT GGTTCGTA

```

+++++

```

Sequence 1      : DREB2D.nuc
Size            : 621
Matching Position : 1 - 621

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatch         : 1
Gaps              : 1
*N+              : 2

Matching          : 47.49 [%]
Weight           : 113

```

```

1 : ATG----- TCAT----- CCA----TAG -----AGCCA----
   ***          ** *      * *   ***          ** *
1 : ATGCCCGAGGA AACGGAAGTC TCGTGGAACA CGAGATGTAG CTGAGATTCT AAGGAAATGG

19 : --AAAGT--A ATG----- -----ATGG TTGGTGCT-A ATAAGAAACA
    * *** * ***          ** * ***** * * * * *
61 : AGAGAGTACA ATGAGCAGAC CGAGGCAGAT TCTTGCATCG ATGGTGGTGG TTCAAACCA

```

```

207 : GTTTAGA--- -GGTGT--- -CGACAAAGG GT-----T TGGG--GGAA ATGGGTTGCT
    *   ***   ** **   * * * * *   *   ****   *   *   *   ***
300 : GAACAGAAAC TTGTCTTTTT CTGGCCACGG GTCGGGTTCT TGGGCTTATA ATAAGAAGCT

250 : GAGATACGTG AACCAGTGAG TCACCGTGGT ---GCAAACT CTAGTCGTAG TAAACGGCTT
    **** * *   * * *   *** ****   *   *   *   *** **   *   * *
360 : -CGATATG-G TTCATGGGT GGACCTTGGT CTCGGCCAGG CAAGTTGT-T CACGAGGTTT

307 : TGGCTTGG-- ----CACGTT TGCTAC-TGC AGCTGAAGCT GCTTTGGCTT ACGACAGAGC
    *   *** *   *   *** * **** *   ** *** * *   *   *   *   *   *
417 : TTGCTCAGAG AGATCGAGTT TTCTACAAGA AGATGATGAT -CATAGTCAT A----ATCGA

360 : TGCTAGT-GT CA--TGTACG GACCCTATGC CAGGTAAAT TTCCCGGAAG ATTTGGGTGG
    * * * * * * * *   ** ** **   **** ** * * *   *   *   *   *
472 : TGTTCTGCTT CAAGTGGTTC GAATCTTTG- TTGGTT--AT TACCTAAACA AAGTGATTCA

417 : GGGAAGGAAG AAGGACG--- AGGAGGCGGA AAGTTCGGGA GGCTATTG-G TTGAAACT-
    *   *** ** **   * *   **   **** ** ** * * *   *** **
529 : CAAGATCAAG -AGACCGTTA ATGCTACGAC TAGTTATGGC GGTGAAGCGG GTGGTGGCTC

472 : AACAAAGCCG GTAATGGCGT GATTGAAACG GAAG--GTGG AAAAG----- ACTATGTAGT
    **   ** * * *   * * * *   *** * * *   *   *   *   *   *
588 : TACGTTAACG TTTTCGACCA ATTTGAAACC AAAGAATTG ATGAGTCAGA ATTATGGATT

```

60/94

Fig. 4-34

+++++

0010181

```

Sequence 1      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

```

```

Matching      : 45.74 [%]
Weight       : 200

```

```

1 : ATGGAAGG A-----A GATAACGGAT CGAAACA--- -GAGCTC--- ----CTCTGC
    ***** * * *   * * *   *****   *** **   ***
1 : ATGGAAGAAG AGCAACCTCC GGCCAAGAAA CGAAACATGG GGAGATCTAG AAAAGGTTGC

42 : TTCTGTTGTA -----TCC TCGAGAAGAC GAAGAAGA-- ----GTGG-T TGAGCCAGTG
    *   ***   ***   ***** * * *   *   ****   *   *   *   *
61 : ATGAAAGGTA AAGGCGGTCC -AGAGAACGC CACGTGTACT TTCCGTGGAG TTAGGCAACG

88 : GAAGCGACGT TA----- CAGAGAT--G GGAG--GAA- -GAAGGA-TT GGCGAGAGCT
    ** * * *   *   ***** *   *** **   *   *** * * *   ***
120 : GACTTGGGGT AAATGGGTGG CTGAGATCCG TGAGCCTAAC CGTGGGACTC GTCTCTGGCT

133 : CGTAGGGTTC AA----- ----GC CAAAGGTT-C GAAGAA----- -AGGTT
    **   *** **   *   * * *   * * *   *   *   *   *   *
180 : CGGCACGTTT AATACCTCGG TCGAGGCCGC CATGGCTTAC GATGAAGCCG CTAAGAAACT

```

```

525 : CTACAATGAA G---ACGCTA ---TTGAGCT TGGCCATGAC AAGA-----
      ***** * * . *** ** * ** * ** *
648 : ATACAATGGA GCTTGGTCTA GGTTTCTGT GGGCAAGAA AAGAAGACGG AACATGACGT

563 : CTCA----- ---GAATCCT ATGACTGATA ATGA-AATA- GT--GAACCC AG-----
      *** * *** * *** * * * * * * * * * *
708 : GTCATCGTCG TGTGGATCGT CGGAC-AACA AGGAGAGTAT GTTGGTTCCT AGTTGCGGCG

602 : --CAGTGAAA TCAGAGGAAG --GTT---AC AGC---TATG ATCGATTCAA A-----
      * * * * * * * * * * * * * * * *
767 : GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTGGAA ATGGATGATC

643 : --TTGGATAA CG--GATTGT TGTATAATGA ACCTCAAAGC TCCAGTTATC ACCA--GGGA
      ***** * * **** * * * * * * * * * *
827 : TTTTGGAGAT TGATGATTTA GGTGTGTTGA TTGGCAAAAA TGGAGATTTC AAGAATTGGT

697 : GGTG-GATTC GATTCATATT TTGAGTATTT CAGATTCTAG
      * * * * * * * * * * * * * *
887 : GTTGGAAGA GTTCAACAT CCATGGAATT --GGTCTGA

```

+++++

```

Sequence 1      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches          : -1
Mismatched       : 1
Gaps             : 1
*N+              : 2

Matching         : 48.72 [%]
Weight           : 93

```

```

1 : AT-----GGA AAAGGAAGAT AACGGATCGA A-AC-AGA-G CTCCTCTGCT TCTGTTGTAT
  ** *** ** * * * * * * * * * * * * * * * *
1 : ATGCCCAGGA AACGGAAG-T CTCG--TGGA ACACGAGATG TAGCTGAGAT TCTAAGGAA-

53 : CCTCGAGAAG ACGAAGAAGA GTGGTTGAGC CAGTGAAGC GACGTTACAG AGATGGGAGG
  * *** * * * * * * * * * * * * * * *
57 : -ATGGAG-AG AGTACAATGA G-----CAGA CCGAGGCAGA TTC-TTGCAT CGATGG----

113 : AAGAAGGATT GGCGAGAGCT CGTAGGGTTC AAGCCAAAGG TTCGAAGAAA GGTTGTATGA
  * * * * * * * * * * * * * * * *
105 : -TGTTGGTTC AAAACCAATC CGAAAGGCTC CTCCAAACG TTCGAGGAAG GGTTGTATGA

173 : GAGGAAAAGG TGGACCAGAG AATCCTGTTT GTCGGTTTAG AGGTGTTTCA CAAAGGGTTT
  *** * * * * * * * * * * * * * * *
164 : AAGGTAAAGG TGGACCTGAA AATGGGATTT GTGACTATAC AGGAGTTAGA CAGAGGACAT

233 : GGGGGAATG GGTGCTGAG ATACGTGAAC CAGTGAGTCA CCGTGGTGCA AACTCTAGTC
  **** * * * * * * * * * * * * * *
224 : GGGGTAAATG GGTGCTGAG ATCCGTGAGC CAG-----G CCGAGGTGC- -----

293 : GTAGTAAACG GCTTTGGCTT GGCACGTTTG CTAAGTGCAG TGAAGCTGCT TTGGCTTACG

```

Fig. 4-35

0010181

```

525 : CTACAATGAA G---ACGCTA ---TTGAGCT TGGCCATGAC AAGA-----
      ***** * *      ***      ** * ** * ** *
648 : ATACAATGGA GCTTGGTCTA GGTTCCTTGT GGGGCAAGAA AAGAAGACGG AACATGACGT

563 : CTCA----- ---GAATCCT ATGACTGATA ATGA-AATA- GT--GAACCC AG-----
      ***      * *** *      *** * * * * * ** * * *
708 : GTCATCGTCG TGTGGATCGT CGGAC-AACA AGGAGAGTAT GTTGGTTCCT AGTTGCGGCG

602 : --CAGTGAAA TCAGAGGAAG --GTT---AC AGC---TATG ATCGATTCAA A-----
      * * * * * ** * * * * * *** * * * * * * * * *
767 : GAGAGAGGAT GCATAGGCCG GAGTTGGAAG AGCGAACAGG ATATTGGAA ATGGATGATC

643 : --TTGGATAA CG--GATTGT TGTATAATGA ACCTCAAAGC TCCAGTTATC ACCA--GGGA
      ***** * * **** * * * **** * * * * * * * *
827 : TTTTGGAGAT TGATGATTTA GGTTCCTTGA TTGGCAAAAA TGGAGATTTC AAGAATTGGT

697 : GGTG-GATTG GATTGATATT TTGAGTATTT CAGATTCTAG
      * * * * * * * * * * * * * * * * *
887 : GTTGGAAGA GTTCAACAT CCATGGAATT --GGTCTGA

```

+++++

```

Sequence 1      : DREB2E.nuc
Size            : 735
Matching Position : 1 - 735

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

## Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 48.72 [%]
Weight       : 93

```

```

1 : AT-----GGA AAAGGAAGAT AACGGATCGA A-AC-AGA-G CTCCTCTGCT TCTGTTGTAT
  **      *** ** ***** * ** * * * * * * * * * *
1 : ATGCCCAGGA AACGGAAG-T CTCG--TGGA ACACGAGATG TAGCTGAGAT TCTAAGGAA-

53 : CCTCGAGAAG ACGAAGAAGA GTGGTTGAGC CAGTGGAAGC GACGTTACAG AGATGGGAGG
    * *** * * * * * * * * * * * * * * * *
57 : -ATGGAG-AG AGTACAATGA G-----CAGA CCGAGGCAGA TTC-TTGCAT CGATGG----

113 : AAGAAGGATT GGCGAGAGCT CGTAGGGTTC AAGCCAAAGG TTCGAAGAAA GGTGTATGA
     * * * * * * * * * * * * * * * * *
105 : -TGGTGGTTC AAAACCAATC CGAAAGGCTC CTCCTAAACG TTCGAGGAAG GGTGTATGA

173 : GAGGAAAAGG TGGACCAGAG AATCCTGTTT GTCGGTTTAG AGGTGTTTGA CAAAGGGTTT
     *** ***** ** * * * * * * * * * * *
164 : AAGGTAAAGG TGGACCTGAA AATGGGATTT GTGACTATAC AGGAGTTAGA CAGAGGACAT

233 : GGGGGAAATG GGTGCTGAG ATACGTGAAC CAGTGAGTCA CCGTGGTGCA AACTCTAGTC
     **** ***** ***** ** * * * * * * *
224 : GGGGTAAATG GGTGCTGAG ATCCGTGAGC CAG-----G CCGAGGTGC- -----

293 : GTAGTAAACG GCTTTGGCTT GGCACGTTTG CTAAGCTGCT TGAAGCTGCT TTGGCTTACG

```

Fig. 4-36

0010181

```

267 : ----TAA--- GTTATGGCTC GGTACTTTCT CTAGTTCATA TGAAGCTGCA TTGGCTTATG
          *** * * ***** ** * * * *** * * * ***** *
353 : ACAGAGCTGC TAGTGTCTAG TACGGACCCT ATGCCAGGTT AAATTTCCCG GAAGATTGCG
          * *** * * * * ***** * * ***** * * *** * *
320 : ATGAGGCTTC CAAAGCTATT TACGGTCAGT CTGCCCGACT CAATCTTCC- -----
          **
413 : GTGGGGGAAG GAAGAAGGAC GAGGAGGCGG AAAGTTCGGG AGGCTATTGG TTGGAAACTA
          ** * * * * ***** * * * *
369 : -----AC -----TGCTG CCACTGTGTC AGGC--TCGG TT----ACT-
          **
473 : ACAAAGCCGG TAATGGCGTG ATTGAAACGG AAGGTGGAAA AGACTATGTA GTCTACAATG
          ** ** * * * * * * * * * *
399 : -----GC--- --ATTTTCTG A-TGAATCTG AAG----- --TTTGT- -----
          **
533 : AAGACGCTAT TGAGCTTGGC CATGACAAGA CTCAGAATCC TATGACTGAT AATGAAATAG
          ** *****
426 : -----GCACG TGAG----- -----GAT A--CAAAT--
          **
593 : TGAACCCAGC AGTGAAATCA GAGGAAGGTT ACAGCTATGA TCGATTCAAA TTGGATAACG
          ** * * * * ***** * * * * * * * * * *
444 : -----GC A--AGATC- -----TGGTT -TTGGTCAGA TC---TCTAA CT---TCTCG
          **
653 : GATTGTTGTA TAATGAACCT CAAAGCTCCA GTTATCACCA GGGAGGTGGA TTCGATTGAT
          ** ** * * * * * * * * * *
480 : CAT--TTCCA AAATG---T TAA--GTCCA ---ATAAC-- -----TGCA TTGG-----
          **
713 : ATTTTGAGTA TTTCAGATTC TAG
          ** *** * * * *
515 : ---TTAAGTT GGGGCGTTAC TAG
  
```

+++++

```

Sequence 1      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834
  
```

```

Sequence 2      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 54.15 [%]
Weight       : 19
  
```

```

1 : ATGG-AGAA- ATCATCCTC- -----AA TGAACAATG GAAG----- -AAGGGTCCT
    **** * * * * * * * * * *
1 : ATGGAAGAAG AGCAACCTCC GGCCAAGAAA CGAAACATGG GGAGATCTAG AAAAGGT--T
    **** * * * * * * * * * *

43 : GCTCG--GGG TAAAGGCGGT CCACAAAACG CTCTTTGTCA GTACCGTGGA GTCAGGCAAA
    ** * * * * * * * * * *
59 : GCATGAAAGG TAAAGGCGGT CCAGAGAACG CCACGTGTAC TTTCCGTGGA GTTAGGCAAC
    **** * * * * * * * * * *

101 : GGAAGTGGGG CAAATGGGTG GCTGAGATCA GAGAGCCCAA GAAGAGGGCA AGACTTTGGC
    *****
  
```

Fig. 4-37

0010181

```

119 : GGACTTGGGG TAAATGGGTG GCTGAGATCC GTGAGCCTAA CCGTGGGACT CGTCTCTGGC
161 : TTGGCTCTTT CGCTACAGCT GAAGAAGCAG CTATGGCTTA TGATGAGGCT GCCTTGAAAC
    * * * * *
179 : TCGGCACGTT TAATACCTCG GTCGAGGCCG CCATGGCTTA CGATGAAGCC GCTAAGAAAC

221 : TCTATGGGCA CGACGCATAC CTCAACTT-- -----ACC TCATCTTCAG C-----
    ***** ** * * * * *
239 : TCTATGGACA CGAGGCTAAA CTCAACTTGG TGCACCCACA ACAACAACAA CAAGTAGTAG

263 : GGAATACAA- ---GACCTTC TCTGAGTAAC ---TC----T C-AGAGGTTC AAATGGGTAC
    * * * * *
299 : TGAACAGAAA CTTGTCTTTT TCTG-GCCAC GGGTCGGGT CTTGGGCTTA TAATAAGAAG

311 : CTTCAAGGAA GTTTAT---- ---ATCTATG TTTCCTTCAT G--TGGTATG CTAAACGTGA
    * * * * *
358 : C-TCGATATG GTTCATGGGT TGGACCTTGG TCTCGGCCAG GCAAGTTGTT CACGAGGTTC

362 : ATGCTCAGCC TAGTGTTCAC ATAATCCAGC AAAGACTAGA AGAACTCAAG AAAACTGGAC
    ***** ** * * * * *
417 : TTGCTCAG-- -AGAGATCGA GTTTTCTA-C AAGAAGATGA TGATCATAGT CATAATCGAT

422 : TTTTATC-TC AA----TCCT ATTCTT--CT AGTTCCT-CC TCCACCGAAT CAAAACTAA
    * * * * *
473 : GTTCGTCTTC AAGTGGTTCG AATCTTTGTT GGTATTACC TAAACAAAGT GATTACAAG

474 : TACTAGCTTT C-TTGATGAG AAGACCAGCA AGGGAGAAAC AGACAAT---- --ATGTTG-
    * * * * *
533 : ATCAAGAGAC CGTTAATGCT ACGACTAGTT ATGGCGGTGA AGGCGGTGTT GGCTCTACGT

527 : -AAGGTGGT- GATC-AGAAG AAACCAGAGA --TCGACCTG ACCGAGTTTC TTCAGCA-AC
    * * * * *
593 : TAACGTTTTT GACCAATTTG AAACCAAGA ATTTGATGAG TCAGA-ATTA TGGATTATAC

581 : TAGGAATCTT G--AAGGAT GAAATGAAG CAGAACCAAG TGAGGTAGCA -GA-GTGTCA
    * * * * *
652 : AATGGAGCTT GGTCTAGGTT TCTTGTGGG CAAGAAAAGA AGACGGAACA TGACGTGTCA

636 : T--TCCCCTC CACCATGGAA CGAGCAAGAA GAAACTGGAA GTCCTTTCAG AACTGAGAAT
    * * * * *
712 : TCGTCGTGTG GATCGTCGGA C-AACAAGGA GA----GTAT GTTGGTTC-- --CT---AGT

694 : TTCAGCTGGG ATACCTGAT CGAGATGCCA AGAAGTAAA CCACAACAT GCAATTTG--
    * * * * *
760 : TCGGCGGAG AGA---GGAT GCATAGGCC- GGAGTTGGA GAGCGAACAG GATATTTGGA

752 : ACTCCAGCAA CTTGGAAGC T--ATGATT- -----TTG A--GG--ATG ATGTATCCTT
    * * * * *
816 : AATGGATGAT CTTTGGAGA TTGATGATT AGGTTTGTG ATTGGCAAAA ATGGAGATT

798 : C---CCTTCC ATCTGGG--- -----ACT ACTACGGAAG CTTAGAT-TG A
    * * * * *
876 : CAAGAATTGG TGTGTGAAG AGTTTCAACA TCCATGGAA- -TTGGTTCTG A
  
```

+++++

```

Sequence 1      : DREB2F.nuc
Size            : 834
Matching Position : 1 - 834

Sequence 2      : DREB2H.nuc
  
```

Fig. 4-38

0010181

Size : 534  
 Matching Position : 1 - 534

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 41.63 [%]  
 Weight : 254

```

1 : ATGGAGAAAT CATCCTCAAT GAAACAATGG AAGAAGGGTC CTGCTCGGGG TAAAGGCGGT
   ***          * * ***** ** ***          **** ** **
1 : ATG----- ----CCCAG GAAAC---GG AAG----- --TCTCGTGG --AA-----

61 : CCACAAAACG CTCTTTGTCA GTACCGTGGA GTCAGGCCAA GGAAGTGGGG CAAATGGGTG
   *** * *          ***          * * * * * * * * * *          *****
29 : -CACGAGA-- ----TGT-- ----AGCTGA G--ATTCTAA GG----- -AATGG--

121 : GCTGAGATCA GAGAGCCCAA GAAGAGGGCA AGACTTTGGC TTGGCTCTTT CGCTACAGCT
       * ***** ** * ***          **** *** * *****
61 : -----A GAGAGTACA- -ATGAG---C AGACCGAGGC -AGATTCTT- -----

181 : GAAGAAGCAG CTATGGCTTA TGATGAGGCT GCCTTGAAAC TCTATGGGCA CGACGCATAC
       *** * ***** ** **          ** *** * * * * * * * * *
95 : -----GCAT CGATGG---- TGGTG----- --GTTCAAAA CCAATCCGAA AGGCTCCT-C

241 : CTCAACTTAC CTCATCTTCA GCGGAATACA AGACCTTCTC TGAGTAACTC TCAGAGGTTG
   * ***          *** * *****          * ** * * * * *
137 : CAAAAC---- ----GTTG- GAGGAA---- ----- -GGGT-TGTA TGAAGGT--

301 : AAATGGGTAC CTTCAAGGAA GTTTATATCT ATGTTTCCTT CATGTGGTAT GCTAA--ACG
   *** * * * * *          *** * * * * * * * * * * * * * *
169 : AAAGGTGGAC CT-----GAA AATGGGATTT GTGACT-ATA CAGGAGTTAG ACAGAGGACA

359 : TGAATGCTCA GCCTAGTGTT CACATAATCC AGCAAAGACT AGAAGAACTC AAGAAAAGTC
   ** * * * *          ** * * * *          *** * * *          *** * * *
223 : TG--GGGTAA ATGGGTGCT GAGATCCGTG AGCCAGGCC- -GAGGTGCT- AAG-----

419 : GACTTTTATC TCAATCCTAT TCTTCTAGTT CTTCCTCCAC CGAATCAAAA ACTAATACTA
   ** * * * * * * * * * *          *          ** ** * * *
271 : ---TTATGGC TCGGTACT-T TC-TCTAGTT C----- --ATATGAA GCT-GCATTG

479 : GCTTTCTTGA TGAGAAGACC AGCAAGGGAG AAACAGACAA TATGTTGAA GGTGGTGATC
   **** *** ***** ** * *** *          ** * * * * * * * *
313 : GCTT--ATGA TGAGGCTTCC A--AAGCTAT TTACGGTCAG TCTGCCCGA- -----C

539 : AGAAGAAACC AGAGATCGAC CTGACCGAGT TTCTTCAGCA ACTAGGAATC TTGAAGGATG
   ** ** * * *          *** **          ** *          *** * * * *
359 : TCAATCTTCC ACTGCTGCCA CTGTGTCAG- --GCTCGGTT ACT--GCATT TT--CTGATG

599 : AAAATGAAGC AGAACCAAGT GAGGTAGCAG AGTGTCATTC CCCTCCACCA TGAACGAGC
   ** *****          ** ** *****          **          **          * **
412 : AATCTGAAGT TTGTGCACGT GAGG----- ----AT-- -----AC-- ----AAATGC

659 : AAGAAGAAAC TGGAAGTCCT TTCAGAACTG AGAATTTGAG CTGGGATACC CTGATCGAGA
   *** * * * *          * ** * * * * * * * *          ** ** ***
446 : AAG-----ATC TGG-----T TTTGG---TC AG-ATCTC-- -----TA-A CTTCTCGCAT

```



Fig. 4-39

0010181

```

719 : TGCCAAGAAG TGAAACCACA ACTATGCAAT TTGACTCCAG CAACTTCGGA AGCTATGATT
      * ****          ***      * * * * *      * * * * *      * * *
483 : TTCCAA----- --AATG--- TTAAGTCCAA TAACT----- -GC---ATT

```

```

779 : TTGAGGATGA TGTATCCTTC CCTTCCATCT GGGACTACTA CGGAAGCTTA GATTGA
      * * * * *      * * * * *      * * * * *      * * *
513 : -----GGTTA AGT-----T GGGGC-GTTA C-----TA G-----

```

+++++

```

Sequence 1      : DREB2G.nuc
Size            : 924
Matching Position : 1 - 924

```

```

Sequence 2      : DREB2H.nuc
Size            : 534
Matching Position : 1 - 534

```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 38.38 [%]
Weight       : 325

```

```

1 : ATGGAAGAAG AGCAACCTCC GGCCAAGAAA CGAAACATGG GGAGATCTAG AAAAGGTTGC
   **          * * * * * * * * * * * * * * * * * * * *
1 : AT----- GCCCAGGAAA CGGAAGTCTC GTGGAAC-AC GAGATGTAGC

61 : ATGAAAGGTA AAGGCGGTCC AGAGAACGCC ACGTGTACTT TCCGTGGAGT TAGGCAACGG
    *** *      **** *      ****          * * * * *      *
42 : -TGAGATTCT AAGGAAATGG AGAGA----- ----GTACAA TGAGCAGACC GAGGCA---G

121 : ACT-TGGGGT AAATGGGTGG CTGAGATCCG TGAGCCTAAC CGTGGGACTC GTCTCTGGCT
    * * * * * * * * * * * * * * * * * * * * * *
89 : ATTCTTGCAT CGAT-GGTGG -TG-GTTC-- AAAACCAATC CGAAAGGCTC -----CT

180 : CGGCACGTTT AATACCTCGG TCGAGGCCGC CATGGCTTAC GATGAAGCCG CTAAGAAACT
    * **      **      * * * * *      * * * * *      * * *
136 : C--CA----- AA----ACGT TCGAGG---- -AAGGGT-- -----GTATGAAA--

240 : CTATGGACAC GAGGCTAAAC TCAACTTGGT GCACCCACAA CAACAACAAC AAGTAGTAGT
    * * * * *      * * * * *      * * * * *      *
166 : -----GGTAAA- -----GGT GGACC-----T

300 : GAACAGAAAC TTGTCTTTTT CTGGCCACGG GTCGGGTTCT TGGGCTTATA ATAAGAAGCT
    **      ***          * * * * *      * * * * *      * * *
181 : GA---AAA- -----TGGGAT-T TGTGACTATA --CAGGAGTT

360 : CGATATGGTT CATGGGTTGG ACCTTGGTCT CGGCCAGGCA AGTTGTTTAC GAGGTTCTTG
    * * * * * * * * * * *      * * * * *      * * * * *
211 : AGACAGAGGA CATGGGGTAA A---TGG--- -GTTGCT--- GAGATCCGTG

420 : CTCAGAGAGA TCGAGTTTTT TACAAGAAGA TGATGATCAT AGTCATAATC GATGTTCTGC
    ** **      ****          * * * * *      * * *
251 : ---AGCCAGG CCGAG-----GTGCTAA-- ---GTT-----

480 : TTCAAGTGGT TCGAATCTTT GTTGGTTATT ACCTAAACAA AGTGATTCAC AAGATCAAGA

```

Fig. 4-40

0010181

```

273 :   ***   ***   ****   *           ***
      -----ATGGC TCGGTACTTT CT----- --CTA-----

540 :   GACCGTTAAT GCTACGACTA GTTATGGCGG TGAAGGCGGT GGTGGCTCTA CGTTAACGTT
      *** *           ****           * * *   ***** ** * * * *
293 :   ----GTTCA- ----- --TATG----- ---AAGCTGC ATTGGCT-TA TGATGAGGCT

600 :   TTCGACCAAT TTGAAACCAA AGAATTTGAT GAGTCAGAAT TATGGATTAT ACAATGGAGC
      *           **** **   ** * *   *****   ** *   ****   *
328 :   T----- --CCAA AGCTATTTAC G-GTCAG--- TCTGCCCGAC TCAAT----C

660 :   TTGGTCTAGG TTTCTTGTGG GGCAAGAAAA GAAGACGGAA CATGACGTGT CATCGTCGTG
      ** ** * * *   ** * * *   ***           * ** **   *** **
365 :   TTCCACT--G CTGCCACTGT GTCAGG----- ---CTCGG-- --TTAC-TG- CATTTTCTGA

720 :   TGGATCGTCG GACAACAAGG AGAGTATGTT GGTTCCTAGT TCGGCGGGAG AGAGGATGCA
      ** ***           * * *** ***           ** *   ***** **
410 :   TGAATC---- -----TG A-AGTTTGT- ----- ---GC-ACG TGAGGATACA

780 :   TAGGCCGGAG TTGGAAGAGC GAACAGGATA TTTGGAAATG GATGATCTTT TGGAGATTGA
      *           ** **** *           ** *   *** *** * **
441 :   AA----- -TGCAAGATC ----- --TG G-----TTT TGGTCA--GA

840 :   TGATTTAGGT TTGTTGATTG GCAAAAATGG AGATTTCAAG AATTGGTGTT GTGAAGAGTT
      * * **   ** * * *   *   *****   * * ***   ** **   * ** ***
466 :   T-CTCTA-AC TTCTCGCATT TCCAAAATGT TAAGTCCAAT AACTGCATTG GTTAAG----

900 :   TCAACATCCA TGGAATTGGT TCTGA
      * *   * * **
520 :   ----- TTGGGGCGTT ACTAG

```



Fig. 5-2

0056504

Matching : 36.83 [%]  
Weight : 128

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS -----TKK
  *               ** **** *   *** * *   **** * *
1 : M----- --PSEIVDRK RKSRTGRD-- -VAEILRQWR EYNEQIEAES CIDGGGPKSI

54 : RKVPAKGSKK GCMKGKGGPE NSRCSFRGVR QRIWGWVAE IREPNGSRL WLGTFTPAQE
  ** * *** * ***** * * **** ** ***** **** * ** ***** *
47 : RKPPPKGSRK GCMKGKGGPE NGICDYRGVR QRRWGWVAE IREPDGGARL WLGTFSSSYE

114 : AASAYDEAAK AMYGPLARLN FPRSDASEVT STSSQSEVCT VETPGCV--- HVKTEDPDCE
  ** ***** * ** **** *   * *   * *   * *   * *   * *
107 : AALAYDEAAK AIYGQSARLN LP-----EIT NRSS-STAAAT ATVSGSVTAF SDESEVCARE

171 : SKPFSGGVEP MYCLENAAE MKRGVKADKH WLSEFEHNYW SDILKEKEKQ KEQGIVETCQ
  * *   ** *   * *   *   *   *   *   *   *   *
161 : DTNASSG-FG QVKLEDCSDE ---YVLLDSS QCIKEE--- ---LKGKEEV REEHNLA VGF

231 : QQQQDS---- LSVADYGWPN DVDQSHLDSS DMFDVDELLR DLNGDDV--- -FAGLNQDRY
  *** *   * *   *   *   *   *   *   *   *
210 : GIGQDSKRET LDAWLMGNGN EQEPLEFGVD ETFDINELLG ILNDNNVSGQ ETMQYQVDRH

283 : P-----G NSVANGSYRP -ESQQSGFD- -----PLQS LNYGIPPFQL EGKD---GNG
  *   ** ** * * * *   *   **** *
270 : PNFSYQTQFP NSNLLGSLNP MEIAQPGVDY GCPYVQPSDM ENYGIDLDRH RFNDLDIQDL

324 : FFDDL SYLDL EN
  *
330 : DFGGDKDVHG ST

```

+++++

Sequence 1 : DREB2A. aa  
Size : 335  
Matching Position : 1 - 335

Sequence 2 : DREB2D. aa  
Size : 206  
Matching Position : 1 - 206

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 28.96 [%]  
Weight : 167

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *               * * *   * * *
1 : M----- --SSIE PKVMMVG--- -----AN KKQRTVQA-S

61 : SKKGCMKGKG GPENSRCFR GVRQRIWGW VAEIREPNRG SRLWLGTFT AQAASAYDE
  * **** ** * *   ***** ***** ***** *   ***
24 : SRKGCMRGKG GPDNASCTYK GVRQRTWGW VAEIREPNRG ARLWLGTFT SREAAALAYS

121 : AAKAMYGLA RLNFPRSDAS EVTSTSSQE VCTVETPGCV HVKTEDPDCE SKPFSGGVEP
  ** *** * * * * *   **   **   * * * *

```

Fig. 5-3

0056504

```

84 : AARKLYGPEA HLNLPESLRS YPKTASS--- PASQTPSSN TGGKSSSDSE S-PCS-----
181 : MYCLENAGEE MKRGVKADKH WLSEFEHNYW SDILKEKEKQ KEQGIVETCQ QQQQDSLSVA
135 : -----SNE M-----S SCGRVTEEIS WEHINV-----DLPVM
241 : DYGWPNDVDQ SHLDSSDMFD VDELLRDLNG DDVFAGLNQD RYPGNSVANG SYRPESQQSG
161 : D-----DSS---I WEEATMSLGF PWVHEGDN-----DISR
301 : FDPLQSLNYG IPPFQLEGKD GNGFFDDLSY LDLEN
188 : FDTGIS-----GGYSNWDSFH SPL--
  
```

+++++

```

Sequence 1      : DREB2A.aa
Size            : 335
Matching Position : 1 - 335

Sequence 2      : DREB2E.aa
Size            : 244
Matching Position : 1 - 244
  
```

Matching Condition.

```

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 34.20 [%]
Weight       : 143
  
```

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  * * * * *
1 : MEKEDNGSKQ SSSASVSSR ---RRRRVVE PVEATLQRW- ----EEGL ARARRVQAKG

61 : SKKGCMKGKG GPENSRCFSR GVRQRIWGKW VAEIREP--- ----NRGSR LWLGTFTPAQ
***** ** * * * * *
52 : SKKGCMRGKG GPENPVCFRF GVRQRVWGKW VAEIREPVSH RGANSRSRKR LWLGTFTATA

113 : EAASAYDEAA KAMYGLARL NFPRSDASEV TSTSSQSEVC TVETPGCVHV KTEDPDCESE
*** ** * * * * *
112 : EAALAYDRAA SVMYGPYARL NFP----- --EDLGGGRK K--DEEAES-

173 : PFSGGVEPMY CLE-NGAEEM KRGVKADKHW LSEFEHNYWS DILKEKEKQK EQGIVETCQQ
*** * * * *
150 : --SGG---Y WLETNKA--- GNGV----- --IETEGGK DYVVYNEDAI ELGHDKT-QN

232 : QQQQDSLSVAD YGWPNDVDQS HLDSSDMFDV DELLRLDNGD DVFAGLNQDR YPGNSVANGS
* * * * *
191 : PMTDNEIV-- ---NPAVKSE EGYSYDRFKL D----- --NGL

292 : YRPESQQSGF DPLQSLNYGI PPFQLEGKDG NGFFDDLSY- LDLEN
* * * * *
220 : LYNEPQSS-- ---SYHQC- ----- -GGFD--SYF EYFRF
  
```

+++++

```

Sequence 1      : DREB2A.aa
Size            : 335
Matching Position : 1 - 335
  
```

Fig. 5-4

0056504

Sequence 2 : DREB2F.aa  
 Size : 277  
 Matching Position : 1 - 277

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 27.71 [%]  
 Weight : 176

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *          *          *          *          *
1 : M----- EKSS----- MKQ

61 : SKKGCMKGKG GPENSRCFSR GVRQRIWGWK VAEIREPNRG SRLWLGTFPT AQEAASAYDE
    *** ** * * * * * * * * * * * * * * * * * * * * * * * * * *
10 : WKKGPARGKG GPQNALCQYR GVRQRTWGWK VAEIREPKKR ARLWLGSFAT AEEAAMAYDE

121 : AAKAMYGLA RLNFPRSDAS EVTSTS-SQ- ----SEVCT VETPGC---- ----VHVKTE
    ** ** * ** * * * * * * * * * * * * * * * * * * * * * *
70 : AALKLYGHDA YLNLPHLQRN TRPSLSNSQR FKWVPSRKFI SMFPSCGMLN VNAQPSVHI I

166 : DPDCESKPFS GGVEPMYCLE NGAEEMKRGV KADKHWLSEF EHNYWSDILK EKEKQKEQGI
    *          *          *          *          *          *          *
130 : QQRLEELKKT GLLSQSYSSS SSSTE----S KTNTSFLDEK TSKGETDNMF EGGDQKKPEI

226 : VETCQQQQQD SLSVADYGWP NDVDQSHLDS SDMFVDVDELL RDLNGDDVFA GLNQDRYPGN
    * ** * * * * * * * * * * * * * * * * *
186 : DLTEFLQQLG ILKDENEAEF SEVAECH--S PPPWNEQEET GSPFRTENFS WDTLIEMP--

286 : SVANGSYRPE SQQSGFDPLQ SLNYGIPPFQ LEGKDGNGFF DDLSYLDLEN
    * *          * * * * * * * * * * *
242 : -----RSE TTTMQFD--- SSNFGSYDF- ---EDDVSFP SIWDYYGSLD
  
```

+++++

Sequence 1 : DREB2A.aa  
 Size : 335  
 Matching Position : 1 - 335

Sequence 2 : DREB2G.aa  
 Size : 306  
 Matching Position : 1 - 306

## Matching Condition.

Matches : -1  
 Mismatches : 1  
 Gaps : 1  
 \*N+ : 2  
 Matching : 26.12 [%]  
 Weight : 184

```

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVEEVS TKKRKVPAGK
  *          *          *          *          *
1 : ----- EEEQ PPAKRRNMGR

61 : SKKGCMKGKG GPENSRCFSR GVRQRIWGWK VAEIREPNRG SRLWLGTFPT AQEAASAYDE
  
```

Fig. 5-5

```

                                0056504
15 : * ***** **** * ** ***** **** ***** **** * *** ****
      SRKGCMKGKG GPENATCTFR GVRQRTWGKW VAEIREPNRG TRLWLGTFNT SVEAAMAYDE

121 : AAKAMYGLA RLN--FPRSD ASEV----TS TSSQSEVCTV ETPGCVHVKT EDPDCESKPF
      *** ** * ** * * * * *
75 : AAKKLYGHEA KNLNVHPQQQ QQVVVNRNLS FSGHSGGSWA YNKKLDMVHG LDLGLGQASC

175 : SGGVEPMYCL ENGAEEMKRG VKADKHWLSE FEHNYWSDIL KEKEKQKEQG IVETCQQQQQ
      * * * * * * * * *
135 : SRG----SCS ERSSFLQEDD DHSHNRCSSS SGSNLCWLLP KQSDSQDQET VNATTSYGGE

235 : DSLSVADYGW PNDVDQSHLD SSDMFDVDEL LRDNGDDVF AGLNQDRYPG NSVANGS---
      * * * * *
191 : GGGGSTLTFS TNLKPKNLMS QNYGLYNGAW SRFLVGQEKK TEHDVSSSCG SSDNKESMLV

292 : -----YR PE-SQQSGFD PLQSLNYGIP PFQLEGKDG- --NGFFDDL S YLDLEN
      * ** * * * *
251 : PSCGGERMHR PELEERTGYL EMDLLEIDD LGLLIGNGD FKNWCCEEFQ HPWNWF

+++++
Sequence 1 : DREB2A. aa
Size : 335
Matching Position : 1 - 335

Sequence 2 : DREB2H. aa
Size : 177
Matching Position : 1 - 177

Matching Condition.
Matches : -1
Mismatches : 1
Gaps : 1
*N+ : 2

Matching : 28.07 [%]
Weight : 170

1 : MAVYDQSGDR NRTQIDTSRK RKSRSRGDGT TVAERLKRWK EYNETVE--- ---EVSTKK
      * ** ***** * *** * * **** *
1 : M-----PRK RKSRTGTRD--VAEILRKWR EYNEQTEADS CIDGGGSKPI

54 : RKVPAKGSKK GCMKGKGPE NSRCSFRGVR QRIWGKWVAE IREPNGSRL WLGTFPTAQE
      * * * * * ***** * * *** ** ***** **** * * *
42 : RKAPPKRSRK GCMKGKGPE NGICDYTGVR QRTWGKWVAE IREPGRGAKL WLGTFSSSYE

114 : AASAYDEAAK AMYGPLARLN FPRSDASEVT STSSQSEVCT VETPGCVHVK TEDPDCESKP
      ** ***** * * * * *
102 : AALAYDEASK AIYQGSARLN LP----- -LLPLC---

174 : FSGGVEPMYC LENGAEEMKR GVKADKHWLS EFEHNYWSDI LKEKEKQKEQ GIVETCQQQQ
      * * * * *
129 : -----QARLL HFLMN---- LK----- -FVHVRIQM

234 : QDSLSVADYG WPNDVDQSHL DSSDMFDVDE LRLDNGDDV FAGLNQDRYP GNSVANGSYR
      * * * * *
150 : DLVL----- -VRSLS RISKMLSPIT AL----- -VKLGRY-

294 : PESQQSGFDP LQSLNYGIPP FQLEGKDGNG FFDDL SYLDL EN
178 : -----

```

Fig. 5-6

0056504

+++++

Sequence 1 : DREB2B.aa  
Size : 330  
Matching Position : 1 - 330

Sequence 2 : DREB2C.aa  
Size : 341  
Matching Position : 1 - 341

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 33.62 [%]  
Weight : 134

```

1 : MAVYEQTGTE QPKKRKSRR AGGLTVADRL KKWKKEYNEIV EASAVKEGEK PK--RKVPAK
  *          ***** * * * * * * * * * * * * * * * *
1 : M-----PSEI VDRKRKSR-- -GTRDVAEIL RQWREYNEQI EAESCIDGGG PKSIRKPPPK

59 : GSKKGCMKGK GGPDSHSCSF RGVQRRIWKG WVAEIREPKI GTRLWLGTFP TAEKAASAYD
  ** ***** * * * * * * * * * * * * * * * *
53 : GSRKGCMKGK GGPENGICDY RGVQRRIWKG WVAEIREPDG GARLWLGTFP SSYEALAYD

119 : EAATAMYGSL ARLNFP---- ------QS VGSEFTSTSS QSEVCTVENK AVVCGDVCVK
  *** * * * * * * * * * * * * * * * * * * *
113 : EAAKAIYGQS ARLNLPEITN RRSSTAATAT VSGSVTAFSD ESEVCAREDT NASSGFGQVK

167 : HEDTDCESNP FSQILDVREE SCG----TRP DSCTVGHQDM NSSLNYDLLL EFEQQYWGQV
  ** * * * * * * * * * * * * * * * *
173 : LEDCSDEYVL LDSSQCIKEE LKGKEEVREE HNLAVGFGIG QDSKRETLDA WLMGNGNEQE

223 : LQE---KEKP KQEE---EEI QQQQQEQQQQ QLQPDLLTVA DYGPWWSNDI VNDQTSWDPN
  * * * * * * * * * * * * * * * *
233 : PLEFGVDETF DINELLGILN DNNVSGQETM QYQVDRHPNF SYQTQFPN-- SNLLGSLNPM

277 : ECFDINELLG DLNEPGPHQS QDQNHVNSGS YDLHPLHLEP HDGHEFNGLS SLDI
  * * * * * * * * * *
291 : E---IAQPGV DYGCPIYQPS DMENYGIDLD HRRFNDLDIQ DLDFGGDKDV HGST
  
```

+++++

Sequence 1 : DREB2B.aa  
Size : 330  
Matching Position : 1 - 330

Sequence 2 : DREB2D.aa  
Size : 206  
Matching Position : 1 - 206

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 28.48 [%]  
Weight : 166



Fig. 5-7

0056504

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPAKGS
  * * * * *
1 : MSSIE----- -PK----- -VMMV GA-----NK KQRTVQA-SS

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREPKIGT RLWLGTFPTA EKAASAYDEA
    **** * * * * *
25 : RKGCMRGKGG PDNASCTYKG VRQRTWGKVV AEIREPNRGA RLWLGTFDTS REAALAYDSA

121 : ATAMYGSLAR LNFPQSVGSE FTSTSSQSEV CTVENKAVVC GDVCVKHEDT DCESNPFQSI
    * * * * *
85 : ARKLYGPEAH LNLPELSRSY PKTASS----- -PASQ-

181 : LDVREESCGT RPDSCVGHG DMNSSLNYDL LLEFEQQYWG QVLQEKEKPK QEEEEIQQQQ
    * * * * *
115 : -----T TPSSNTGG-- -KSSSDSESP CSSNEMSSCG RV----- -TEEI-

241 : QEQQQQQLQP DLLTVADYGW PWSNDIVNDQ TSWDPNECFD INELLGDLNE PGPHQSQDQN
    * * * * *
149 : ----SWEHIN VDLPMDDSS IWEEATMSLG FPWVHEGDND I--SRFDTCI SGGYSNWDSF

301 : HVNSGSYDLH PLHLEPHDGH EFNGLSSLDI
    * * * * *
203 : H----- -SPL-

```

+++++

```

Sequence 1      : DREB2B.aa
Size            : 330
Matching Position : 1 - 330

Sequence 2      : DREB2E.aa
Size            : 244
Matching Position : 1 - 244

```

## Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching         : 29.20 [%]
Weight           : 161

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPAKGS
  * * * * *
1 : M-EKEDNG-- --SKQSSA-- --SVVSSRRR RRVVEPVEAT LQRWEEGLA RARRVQAKGS

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREP----- -KIGTRL WLGTFTAEK
    ***** * * * * *
53 : KKGCMRGKGG PENPVCFRFG VRQVWGKVV AEIREPVSHR GANSSRSKRL WLGTFTAAE

113 : AASAYDEAAT AMYGSLARLN FPQSVGSEFT STSSQSEVCT VENKAVVCGD VCVKHEDTDC
    ** *** ** * * * * *
113 : AALAYDRAAS VMYGPYARLN FP-----

173 : ESNPFQILD VREESCGTRP DSCTVGHQDM NSSLNYDLLL EFEQQYWGQV LQEKEKPKQE
    * * * * *
135 : EDLGGGRKKD EEAESSG--- -GYWL ETNKAGNGVI ETEGKDYVV

233 : EEEIQQQQQE QQQQLQPD LTVADYGPW SNDIVNDQTS WDPNECFDIN ELLGDLNEPG

```

Fig. 5-8

```

                                0056504
176 : YNEDAIELGH DKTQNPMTD- ----- * *** * * *
                                * * *
293 : PHQSQQNHV NSGSYDLHPL HLEPHDGHEF -NGLSSLDI
                                * * *
220 : -----LYNEP QSSSY----- ----HQQGGF DSYFEYFRF

++++++

Sequence 1      : DREB2B.aa
Size           : 330
Matching Position : 1 - 330

Sequence 2      : DREB2F.aa
Size           : 277
Matching Position : 1 - 277

Matching Condition.

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 28.06 [%]
Weight       : 163

1 : MAVYEQTGTE QPKKRKSRR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPAKGS
  : M----- **
  : EK ---SSSMKQW

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGWV AEIREPKIGT RLWLGTFPTA EKAASAYDEA
    : *** **
11 : KKGPARCKGG PQNALCQYRG VRQRTWGWV AEIREPKKRA RLWLGSFATA EEAAMAYDEA

121 : ATAMYGSLAR LNFPQSVGSE FTSTS-SQSE VCTVENKAVV CGDVCVKHED TDCESNPFQ
    : * ** * ** *
71 : ALKLYGHDAY LNLPHLQRNT RPSLSNSQRF KWVPSRKFI MFPSGMLNV NAQPSVHIQ

180 : ILDVREESCG TRPDCTVGH QDMNSSLNYD LLEFEQQYW GQVLQEKEKP KQEEEEIQQ
    : * * *
131 : QRLEELKKTG LLSQSYSSSS SSTESKTNTS FL--DEKTSK GETDNMFEGG DQKKPEIDLT

240 : QQEQQQQQL- ---QPDLLTV ADYGWPWSND IVNDQTSWDP NECFDINELL GDLNEPGPHQ
    : ** * * *
189 : EFLQQLGILK DENEAPSEV AECHSPPWN EQEETGSPFR TENFSWDTLI EMRSETTTM

296 : SQDQNHVNSG SYDLHPLHLE PHDGHEFNGL SSLDI
    : * * *
249 : QFD--SSNFG SYDFEDDVSF P---SIWDYY GSLD-

```

```

++++++

Sequence 1      : DREB2B.aa
Size           : 330
Matching Position : 1 - 330

Sequence 2      : DREB2G.aa
Size           : 306
Matching Position : 1 - 306

Matching Condition.

Matches      : -1
Mismatches   : 1

```

Fig. 5-9

0056504

```

Gaps          :      1
*N+           :      2

Matching      :    26.35 [%]
Weight       :    185

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EASAVKEGK PKRKVPKGS
   * **
1 : -----EEE QP----- PAKKRNMGSR

61 : KKGCMKGKGG PDNSHCSFRG VRQRIWGKVV AEIREPKIGT RLWLGTFPTA EKAASAYDEA
    ***** * * * *** **** * * * * * * * * * * * * * * * *
16 : RKGCMKGKGG PENATCTFRG VRQRTWGKVV AEIREPNRGT RLWLGTFNTS VEAAMAYDEA

121 : ATAMYGLSLAR LN--FPQSVG SEFTSTSSQS EVCTVENKAV VCGDVCVKHE DTDCESNPFS
    * ** * ** **
76 : AKKLYGHEAK LNLVHPQQQQ QVVVNRNLSF SGHSGSGWAY NKKLDMVHGL DLGLGQASCS

179 : QILDVREESC GTRPDSCTVG HQDMSSSLNY DLLLEFEQQY WGQVLQEKEK PKQEEEEIIQQ
    * * * * * * * * * *
136 : -RGSCSERSS FLQED-DDHS HNRCSSSSGS NLCWLLPKQS DSQDQETVNA TTSYGGEGGG

239 : QQEQQQQQQL QPDLLTVADY G---WPWS-- -----N DIVNDQTSWD PNECFDINEL
    * * * * * * * * * *
194 : GSTLTFSTNL KPNLMSQNY GLYNGAWSRF LVGQEKKTEH DVSSSCGSSD NKESMLVPSC

285 : LG---DLNEP GPHQSQQDNH VNSGSYDLHP LHLEPHD--- -GHEFNGLSS LDI
    * * * * * * * * * *
254 : GGERMHRPEL EERTGYLEMD DLLEIDDLGL LIGKNGDFKN WCCEEFQHPW NWF

```

+++++

```

Sequence 1      : DREB2B.aa
Size            :    330
Matching Position :    1 -    330

```

```

Sequence 2      : DREB2H.aa
Size            :    177
Matching Position :    1 -    177

```

Matching Condition.

```

Matches        :    -1
Mismatches     :     1
Gaps           :     1
*N+            :     2

Matching       :    28.92 [%]
Weight        :    160

```

```

1 : MAVYEQTGTE QPKKRKSRAR AGGLTVADRL KKWKEYNEIV EA--SAVKEG EKP RKVPK
   * ***** * * * * * * * * * *
1 : M----- -PRKRKSR-- -GTRDVAEIL RKWREYNEQT EADSCIDGGG SKPIRKAPK

59 : GSKKGCMKGK GGPDSHCSF RGVRQRIWGK WVAEIREPKI GTRLWLGTFP TAEKAASAYD
    * ***** * * * * * * * * * *
48 : RSRKGCMKGK GGPENGICDY TGVRQRTWGK WVAEIREPGR GAKLWLGTF S SYEAALAYD

119 : EAATAMYGLSL ARLNFPQSVG SEFTSTSSQS EVCTVENKAV VCGDVCVKHE DTDCESNPFS
    * * * * *
108 : EASKAIYGQS ARLNLP-----

```

Fig. 5-10

0056504

```

179 : QILDVREESC GTRPDSCTVG HQDMNSSLNY DLLLEFEQQY WGQVLQEKEK PKQEEEEIQQ
124 : ----- --LLPLCQ-- -ARLLHFLMN LKFVHVRIQM

239 : QQEQQQQQQL QPDLLTVADY GWPWSNDIVN DQTSWDPNEC FDINELLGDL NEPGPHQSQD
    *      **      *      *      *      *
149 : Q----- --DL----- --VLVR SLTS----- -RISKML--- -----SPI

299 : QNHVNSGSYD LHPLHLEPHD GHEFNGLSSL DI.
    * * *
169 : TALVKLGRY- -----
  
```

+++++

```

Sequence 1      : DREB2C.aa
Size            : 341
Matching Position : 1 - 341
  
```

```

Sequence 2      : DREB2D.aa
Size            : 206
Matching Position : 1 - 206
  
```

Matching Condition.

```

Matches          : -1
Mismatch          : 1
Gaps              : 1
*N+              : 2

Matching          : 29.03 [%]
Weight           : 167
  
```

```

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCMK
  * *              **      *      *      *****
1 : MSS----- -IEPKVMMVG ANKK--QRTV QASSRKGCMR

61 : GKGGPENGIC DYRGVRQRRW GKWVAEIREP DGGARLWLGT FSSSYEAALA YDEAAKAIYG
  ***** * * * ***** * ***** * * ***** ** ** **
31 : GKGGPDNASC TYKGVQRQRTW GKWVAEIREP NRGARLWLGT FDTSCREAALA YDSAARKLYG

121 : QSARLNLPEI TNRSSSTAAT ATVSGSVTAF SDESEVCARE DTNASSGFGQ VKLEDSCSDEY
    * *****      * ** * *      * ** *
91 : PEAHLNLPE- ----- SLRSYPKTAS SPAS----- QTPSSNTG- --GKSSSD--

181 : VLLDSSQCIK EELKGKEEVR EEHNLAVGFG IGQDSKRETL DAWLMGNGNE QEPLEFGVDE
    * *      *      * **
129 : ---SESPCSS NEMSSCGRVT EE----- -----IS

241 : TFDINELLGI LNDNNVSGQE TMQYQVDRHP NFSYQTQFPN SNLLGSLNPM EIAQPGVDYG
    ** *      *      **      *
150 : WEHINVDLPV MDDSSIWEEA TM----- --SL--- -----G

301 : CPYVQPSDME NYGIDLHRR FNDLDIQDLD FGGDKDVHGS T
    * *      * * * * *      * *
175 : FPWV----- -HEGDNDISR F-DTCISGGY SNWD-SFHSP L
  
```

+++++

```

Sequence 1      : DREB2C.aa
Size            : 341
Matching Position : 1 - 341
  
```

Fig. 5-11

Sequence 2 : DREB2E.aa  
Size : 244  
Matching Position : 1 - 244

0056504

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 30.29 [%]  
Weight : 172

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEA-ESCID GGGPKSIRKP PPKGSRKGCM  
\* \* \* \* \*  
1 : MEKEDNGSKQ SS---SASVV SSRRRRRVVE PVEATLQRWE EEGLARARRV QAKGSKKGCM  
  
60 : KGKGGPENGI CDYRGVRQRR WGWVVAEIRE P--DGGA--- ---RLWLGTF SSSYEALAY  
\*\*\*\*\* \* \*\*\*\*\* \*  
58 : RGKGGPENPV CRFRGVRQRV WGWVVAEIRE PVSHRGANSS RSKRLWLGTF ATAAEAALAY  
  
112 : DEAAKAIYGQ SARLNLPEIT NRSSSTAATA TVSGSVTAFS DESEVCARED TNASSGFGQV  
\* \* \* \* \*  
118 : DRAASVMYGP YARLNFPE-- ----- -DLGGGRKKD EEAE----- ---SSG-----  
  
172 : KLEDCSDEYV LLDSSQCIKE ELKGKEEVRE EHNLA VGFGI GQDSKRETLD AWLMGNGNEQ  
\* \* \* \* \*  
152 : -----GYW L----- ETNKA---GN G---VIETEG GKDYVVYNE-  
  
232 : EPLEFGVDET FDINELLGIL NDNVSGQET MQYQVDRHPN FSQTQFPNS NLLGSLNPME  
\* \* \* \* \*  
179 : DAIELGHDKT QNPMTDNEIV NPAVK---E EGYSYDR--- -----FKLD N-----  
  
292 : IAQPGVDYGC PYVQPSDMEN YGIDLHRRF NOLDIQDLDF GGDKDVHGST  
\* \* \* \* \*  
218 : ---GLLYNE P--QSSSYHQ GG----- --GFDSYF -----EYFRF

+++++

Sequence 1 : DREB2C.aa  
Size : 341  
Matching Position : 1 - 341

Sequence 2 : DREB2F.aa  
Size : 277  
Matching Position : 1 - 277

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 29.89 [%]  
Weight : 172

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PPKGSRKGCMK  
\* \* \* \* \*  
1 : M----- --EKS---SS MKQWKGPAP  
  
61 : KGKGGPENGI CDYRGVRQRRW GKWVVAEIREP DGGARLWLGTF FSSSYEAALA YDEAAKAIYG  
\*\*\*\*\* \* \*\*\*\*\* \* \*\*\*\*\* \* \* \* \* \*

Fig. 5-12

```

                                0056504
17 : GKGGPQNALC QYRGVRQRTW GKWVAEIREP KKRARLWLGS FATAEEAAMA YDEAALKLYG

121 : QSARLNLP-- -EITNRSSST AATATVSGSV TAFSDESEVC AREDTNA--S SGFGQVKLED
      * ****      * * *      * *      * * *      * * *
77 : HDAYLNPLHL QRNTRPSLSN SQRFKWVPS- RKFISMFPSC GMLNVNAQPS VHIIQQRLE-

176 : CSDEYVLLDS SQCIKEELKG KEEVREEHNL AVFGGIGQDS KRETLDALWM GNGNEQEPL
      ** **      * *      * * *      * * *      * * *
135 : ELKKTGLL-- SQ-----SYS SSSSSTESKT NTSFLDEKTS KGET---DNM FEGGDQKKPE

236 : FGVDETFDIN ELLGILNDNN VSGQETMQYQ V-DRHPNFSY QTQFPNSNLL GSLNPMEIAQ
      * *      **** * *      * *      * *      * *
185 : --IDLT-EFL QQLGILKDEN ----EAEPSE VAECHSPPPW NEQ----EET GSPFRTENFS

295 : PGVDYGCPIYV QPSDMENYGI DLDHRRFNDL DIQDLDFGGD KDVHGS-T
      * *      * *      * *      * *      * *
234 : WDTLIEMPRS ETTMQFDSS NFGSYDFED- ---DVSFPSI WDYYGSLD

++++++

Sequence 1      : DREB2C.aa
Size            : 341
Matching Position : 1 - 341

Sequence 2      : DREB2G.aa
Size            : 306
Matching Position : 1 - 306

Matching Condition.

Matches      : -1
Mismatches   : 1
Gaps         : 1
*N+          : 2

Matching      : 28.25 [%]
Weight       : 174

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCMK
1 : ----- * * * ----- * *****
      EEE QPPA----- KKRN MGRSRKGCMK

61 : GKGGPENGIC DYRGVRQRRW GKWVAEIREP DGGARLWLGT FSSSYEAALA YDEAAKAIYG
      ***** * ***** * ***** * ***** * * * * ***** **
22 : GKGGPENATC TFRGVRQRTW GKWVAEIREP NRGTRLWLGT FNTSVEAAMA YDEAAKKLYG

121 : QSARLNLP--- ----PEITNR SSSTAATATV SGSVTAFSDE SEVCAREDTN ASSGFGQVKL
      * ***      ** *      * *      * *      * *
82 : HEAKLNLVHP QQQQVVVNR NLSFSGHGSW SWAYNKKLDM VHGLDLGLGQ ASCSRG-SCS

174 : EDCSDEYVLL DSSQCIKEEL KGKEEVREEH NLAVGFGIGQ DS-KRETLD --WLMGNGNE
      * *      * *      * *      * *      * *      * *
141 : ERSSFLQEDD DHSHNRCSSS SG-----S NLCWLLPKQS DSQDQETVNA TTSYGGEGGG

231 : QEPLEF-GVD ETFDINELLG ILNDNNVSGQ ETMQYQVDRH PNFSYQTQFP N--SNLLGSL
      * *      * *      * *      * *      * *      * *
194 : GSTLTFSTNL KPNKLMSONY GLYNGAWSRF LVGQEKKTEH DVSSSCGSSD NKESMLVPSC

288 : NPMEIAQPGV DYGCPIYVQS DMENYIDLD HRRFNDLDIQ DLDFGGDKDV HGST
      * *      * *      * *      * *
254 : GGERMHRPEL EERTGY-LEM DDLLEIDDLG LLIKNKDFK NWCCEEFQHP WNW

```

Fig. 5-13

0056504

+++++

Sequence 1 : DREB2C.aa  
Size : 341  
Matching Position : 1 - 341

Sequence 2 : DREB2H.aa  
Size : 177  
Matching Position : 1 - 177

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 38.42 [%]  
Weight : 97

```

1 : MPSEIVDRKR KSRGTRDVAE ILRQWREYNE QIEAESCIDG GGPKSIRKPP PKGSRKGCMK
** *** ***** ** * * * * *
1 : MP-----RKR KSRGTRDVAE ILRKWREYNE QTEADSCIDG GGSKPIRKAP PKRSRKGCMK

61 : GKGGPENGIC DYRGVRQRW GKWVAEIREP DGGARLWLGT FSSSYEAALA YDEAAKAIYG
***** ** * * * * *
56 : GKGGPENGIC DYTGVRQRTW GKWVAEIREP GRGAKLWLGT FSSSYEAALA YDEASKAIYG

121 : QSARLNLPEI TNRSSSTAAT ATVSGSVTAF SDESEVCARE DTNASSGFGQ VKLEDCSDEY
*****
116 : QSARLNLP-----

181 : VLLDSSQCIK EELKGKEEVR EEHNLAVGFG IGQDSKRETL DAWLMGNGNE QEPLEFGVDE
** * * *
124 : -LLPLCQ----- -ARL----- -LHF-----

241 : TFDINELLGI LNDNNVSGQE TMQYQVDRHP NFSYQTQFPN SNLLGSLNPM EIAQPGVDYG
* * * * *
136 : -----LMN LKFVHVRIQ- -MQDLV----- -LVRSL-----

301 : CPYVQPSDME NYGIDLHRR FNDLDIQDLD FGGDKDVHGS T
* * * *
158 : --TSRISKM- -----LS PITALVKLGR Y

```

+++++

Sequence 1 : DREB2D.aa  
Size : 206  
Matching Position : 1 - 206

Sequence 2 : DREB2E.aa  
Size : 244  
Matching Position : 1 - 244

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 35.20 [%]  
Weight : 96

Fig. 5-14

0056504

```

1 : M-----SS-IEPKVMMVG A----- NKKQRTVQA-SSRKGCMRGK
   *      **      * * *      * * * *
1 : MEKEDNGSKQ SSSASVVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK

33 : GGPDNASCY KGVQRQWVGK WVAEIREP--NRGA-----RLWLGTFDTS REAALAYDSA
   *** * *      ***** **      ***** *
61 : GGPENPVCRF RGVQRVWVGK WVAEIREPVS HRGANSSRSK RLWLGTFATA AEAALAYDRA

85 : ARKLYGPEAH LNPESLSY PKTASSPASQ TTPSSNTGCK SSSDESPCS SNEMSSCGRV
   * *** * * * * * * * * * * * * *
121 : ASVMYGPYAR LNFPEDLGGG RKKDEEAESS GGYWLETNKA GNGVIE----TEGGKDYVV

145 : TEE--ISWEH INVDPVMD SSIWEEATMS --LGFVWVHE GDNDISRFDT CIS---GGY
   * * *      * * * * * * * * *
176 : YNEDAIELGH DKTQNP-MTD NEIVNPAVKS EEGYSYDRFK LDNGLLYNEP QSSSYHQGGG

197 : SNWDSFHSPL

235 : FDSYFEYFRF

```

+++++

```

Sequence 1      : DREB2D.aa
Size            : 206
Matching Position : 1 - 206

```

```

Sequence 2      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*#+             : 2

Matching          : 32.65 [%]
Weight           : 129

```

```

1 : MSSIEPKVMM VGANKKQRTV QASSRKGCMR GKGGPDNASC TYKGVQRQW GKWVAEIREP
   * * *      **      * * * * * * * *
1 : M---EKSSSM ----KQ--- ---WKKGPAR GKGGPQNALC QYRGVQRQW GKWVAEIREP

61 : NRGARLWLTG FDTSREAALA YDSAARKLYG PEHLNLP-- ----ESL-- ----RSYP
   ***** * * * * * * * * * *
47 : KKRARLWLTG FATAEEAAMA YDEAALKLYG HDAYLNLP HL QRNTRPSLSN SQRFKWVPSR

106 : KTASSPAS-- ----QTPS- ----SNTGGKS--- SSDSESPCS- ----SNEMS
   * * *      **      * * * * *
107 : KFISMFPSCG MLNVNAQPSV HIIQRLLEEL KKTGLLSQSY SSSSSSTESK TNSFLDEKT

140 : -----SC G-----R VTEEISWEHI NVDLPVMD SSIW-----EATMSL
   *      * * * * * * *
167 : SKGETDNMFE GGDQKKPEID LTFELQLGI LKDENEAEPS EVAECHSPPP WNEQEETGSP

174 : GFPVWHEGDN DI-----SRFDTCSIG GY-----SNWDSFHSPL
   * *      * * * *
227 : FRTENFSWDT LIEMPRSETT TMQFDSSNFG SYDFEDDVSF PSIDWYIGSL D

```

+++++



Fig. 5-15

0056504

Sequence 1 : DREB2D.aa  
Size : 206  
Matching Position : 1 - 206

Sequence 2 : DREB2G.aa  
Size : 306  
Matching Position : 1 - 306

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 32.08 [%]  
Weight : 144

```

1 : MSSIEPKVMM VGANKKQRTV QASSRKGCMR GKGGPDNASC TYKGVQRQRTW GKWVAEIREP
    *      **      *****      *      *      *      *      *      *      *
1 : EEQPP-----AKK--RN MGRSRKGCMK GKGGPENATC TFRGVQRQRTW GKWVAEIREP

61 : NRGARLWLG FDSREAALA YDSAARKLYG PEHLNL-----
    *** ***** * ** * ** * ** * ** * ** *
52 : NRGTRLWLG FNTSVEAAMA YDEAAKLYG HEAKLNLVHP QQQQVVVNR NLSFSGHGSG

98 : ----- PESLRSYPKT AS-SPASQTT PSS-----NTGGKSS -----
    *      *      *      *      *      *      *      *
112 : SWAYNKKLDM VHGLDLGLGQ ASCSRGSCSE RSSFLQEDDD HSHNRCSSSS GSNLCWLLPK

127 : -SDS-----ES PCSS-----NEMS-----S CGRVTEEISW
    ***      *      *      *      *      *      *      *
172 : QSDSQDQETV NATTSYGEG GGGSTLTFT NLKPKNLMSQ NYGLYGAWS RFLVGQEKKT

151 : EHINVDLPYM DDSSIWEE--ATMSLGFPPV H-----EGD-----N DISRFDTGIS
    ** *      ** *      *      *      *      *      *
232 : EH--DVSSS CGSSDNKESM LVPSCGGERM HRPELEERTG YLEMDDLLEI DDLGLLIGKN

194 : GGYSNW--DS FHSP---L
    *      *      *      *
289 : GDFKNWCCEE FQHPWNWF

```

+++++

Sequence 1 : DREB2D.aa  
Size : 206  
Matching Position : 1 - 206

Sequence 2 : DREB2H.aa  
Size : 177  
Matching Position : 1 - 177

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 32.03 [%]  
Weight : 101

```

1 : M-----SSIEPK-----VMMVGANKK QR-TVQASSR KGCMRGKGGP
    *      *      *      *      *      *      *
1 : MPRKRKSRGT RDVAEILRKW REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCMKGKGGP

```

Fig. 5-16

0056504

```

36 : DNASCYKGV RQRTWGKWA EIREPNRGAR LWLGTFTSR EAALAYDSAA RKLYGPEAHL
    * * * * * ***** * * * * *
61 : ENGICDYGV RQRTWGKWA EIREPGRGAK LWLGTFSY EAALAYDEAS KAIYQSARL

-96 : NLPESLRYP KTASSPASQT TPSSNTGGKS SSDSESPCSS NEMSSCGRVT EEISWEHINV
    **      *      *      *      *
121 : NL-----P LLPLCQARLL HFLMN--LKF VHVRIQMQL VLVR---LT SRIS-----

156 : DLPVMDSSI WEEATMSLGF PWVHEGDNDI SRFDTCSGG YSNWDSFHSP L
    * *      *      *
163 : ---KMLSPI --TALVKLG- -----R Y

```

+++++

```

Sequence 1      : DREB2E.aa
Size            : 244
Matching Position : 1 - 244

```

```

Sequence 2      : DREB2F.aa
Size            : 277
Matching Position : 1 - 277

```

Matching Condition.

```

Matches          : -1
Mismatches       : 1
Gaps             : 1
*N+              : 2

Matching          : 27.52 [%]
Weight           : 173

```

```

1 : MEKEDNGSKQ SSSASVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK
    ***      ***
1 : MEK----- SSS----- -----MK QWKKGPARGK

61 : GGPENPVCRF RGVQRVWVGK WVAEIREPVS HRGANSSRSK RLWLGTFFATA AEAALAYDRA
    *** * * ***** * * * * *
19 : GGPQNALCQY RGVQRVWVGK WVAEIREP-- -----KKRA RLWLGSFATA EEAAMAYDEA

121 : ASVMYGPYAR LN----- -----FP-----
    * * * * *
71 : ALKLYGHDAY LNLPHLQNT RPSLSNSQRF KWVPSRKFI MFPSGMLNV NAQPSVHIQ

135 : ---EDLGGG RKKDEEAESS GGYWLETN-- -----KAGN GVIETEGG-- -KDYVVYNED
    * *      * *
131 : QRLEELKKTG LLSQSYSSSS SSTESKTNTS FLDEKTSKGE TDNMFEGGDQ KKPEIDLTEF

180 : AIELGHDKTQ N---PMTDNE --IVNPAVKS EEGYSYDR-F KLDNGLLYNE PQS-----
    ** * * * *
191 : LQLGLILKDE NEAEPSEVAE CHSPPPWNEQ EETGSPFRTE NFSWDTLIEM PRSETTTMQF

227 : -SSYHQGGGF --DSYF---- --EYFRF
    **      * *
251 : DSSNFGSYDF EDDVSFPSIW DYYGSLD

```

+++++

```

Sequence 1      : DREB2E.aa
Size            : 244

```

Fig. 5-17

0056504

Matching Position : 1 - 244  
Sequence 2 : DREB2G.aa  
Size : 306  
Matching Position : 1 - 306

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 25.07 [%]  
Weight : 197

```

1 : MEKEDNGSKQ SSSASVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK
1 : ----- ** * * **** **
61 : GGPENPVCRF RGVQRVWGK WVAEIREPVS HRGANSSRSK RLWLGTfATA AEAALAYDRA
24 : GGPENATCTF RGVQRWTGK WVAEIREP-- ----NRGT RLWLGTfNTS VEAAMAYDEA
121 : ASVMYGPYAR LN-----FPE DLGGG-----
76 : AKKLYGHEAK LNLVHPQQQQ QVVVNRNLSF SGHSGSWAY NKKLDMVHGL DLGLGQASCS
141 : RKKDEEAES-----SGG YWL-----ETNKA--GNGV
136 : RGSCSERSSF LQEDDDHSHN RCSSSSGSNL CWLLPKQSDS QDQETVNATT SYGGEggGGS
165 : IET-----EGGKDYVV YN-----EDAIELGHDK TQNPMTDNEI VNPVKSEEG
196 : TLTFSTNLKP KNLMsQNYGL YNGAWSRFLV GQEKTEHDV SSSCGSSDNK ESMLVPSCGG
208 : YSYDRFKL--DNG LLYNEPQSSS YHQGGGFDSY FEYF----R F
256 : ERMHRPELEE RTGYLEMDDL LEIDDLGLLI GKNGDFKNWC CEEFQHPWNW F

```

+++++

Sequence 1 : DREB2E.aa  
Size : 244  
Matching Position : 1 - 244

Sequence 2 : DREB2H.aa  
Size : 177  
Matching Position : 1 - 177

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 29.92 [%]  
Weight : 114

```

1 : MEKEDNGSKQ SSSASVSSR RRRRVVEPVE ATLQRWEEEG LARARRVQAK GSKKGCMRGK
1 : MPRKRKSRGT RDVA--EILR KWREYNEQTE A-DSCIDGGG SKPIRKAPPK RSRKGCМКGK

```

Fig. 5-18

0056504  
61 : GGPENPVCRF RGVQRVWGK WVAEIREPVS HRGANSSRSK RLWLGTFATA AEAALAYDRA  
\*\*\*\*\* \* \*\*\*\*\* \*\*\* \*\*\*\*\* \*  
58 : GGPENGICDY TGVQRRTWGK WVAEIREP-- GRGA----- KLWLGTFSSS YEAALAYDEA

121 : ASVMYGPYAR LNFPELGGG RKKDEEAESS GGYWLETNKA GNGVIEGEG KDVVYVNEDA  
\*\* \*\* \* \* \* \*  
110 : SKAIYGQSAR LNLP-LLPLC QAR----- --LLHFLMN LKFVHVRIQM QDLV-----

181 : IELGHDKTQN PMTDNEIVNP AVKSEEGYSY DRFKLDNGLL YNEPQSSSYH QGGGFDSYFE  
\* \* \* \*  
153 : --LVRSLTSR ISKMLSPITA LVK-----

241 : YFRF

\*  
174 : LGRY

+++++

Sequence 1 : DREB2F.aa  
Size : 277  
Matching Position : 1 - 277

Sequence 2 : DREB2G.aa  
Size : 306  
Matching Position : 1 - 306

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
Matching : 31.41 [%]  
Weight : 138

1 : ME-----KSS SMKQWKKGPA RGKGGPQNAL CQYRGVRQRT WGWVVAEIRE PKKRARLWLG  
\* \* \* \* \*  
1 : EEEQPPAKKR NMGRSRKGCM KGKGGPENAT CTFRGVRQRT WGWVVAEIRE PNRGTRLWLG

56 : SFATAEEAAM AYDEAALKLY GHDAYLNLPH LQ-----RN TRPSLSNSQR FKWVPSRKFI  
\* \* \* \* \*  
61 : TFNTSVEAAM AYDEAALKLY GHEAKLNLVH PQQQQQVVVN RNLSFSGHGS GSW-AYNKKL

110 : SMFPSCGMLN VNAQPSVHII QQRLEELKKT GLLSQSYSSS SS-----STE SKTNTSFLDE  
\* \* \* \* \*  
120 : DMVHGLDLGL GQASCSRGSC SERSSFLQED DDHSHNRCSS SSGSNLCWLL PKQSDS-QDQ

165 : KTSKGETDNM FEGG----- --DQKKP--- --EIDLTEF LQQLGILKDE NEAEPSEVAE  
\* \* \* \* \*  
179 : ETVNATTSYG GEGGGGSTLT FSTNLKPKNL MSQNYGLYNG AWSRFLVGQE KKEHDVSSS

211 : CHS---PPPWN EQEETGS--P FRTENFSWDI LIEM-PRSET TTMQFDSSNF GSYDFEDDVS  
\* \* \* \* \*  
239 : CGSSDNKESM LVPSCGGERM HRPELEERTG YLEMDLLEI DDLGLLIGKN GDFKNWCCEE

266 : FPSIWYYGS LD

\* \*  
299 : FQHPW----N WF

+++++

Fig. 5-19

0056504

Sequence 1 : DREB2F.aa  
Size : 277  
Matching Position : 1 - 277

Sequence 2 : DREB2H.aa  
Size : 177  
Matching Position : 1 - 177

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 21.52 [%]  
Weight : 192

```

1 : M---EKS--- -----SSMKQWK KGPARGKGGP
   *  **
1 : MPRKRKSRGT RDVAEILRWK REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCMKGKGGP

22 : QNALCQYRGV RQRTWGWVA EIREPKRAR LWLGSFATAE EAAMAYDEAA LKLYGHDAYL
    * * * * *
61 : ENGICDYTG V RQRTWGWVA EIREPGRGAK LWLGTFSY EAALAYDEAS KAIYGQSARL

82 : NLPHLQRNTR PSLSNSQRFK WVPSRK FISM FPSCGMLNVN AQPSVHIQQ RLEELKKTGL
    *** * * * *
121 : NLPLLPLCQA RLLHFLMLNK FV-----HVRIQMQ DL-----V

142 : LSQSYSSSSS STESKTNTSF LDEKTSKGET DNMFEQGDQK KPEIDLTEFL QQLGILKDEN
    * * * * *
153 : LVRSLTSRIS KMLS-----PITAL VKLG-----

202 : EAEPSEVAEC HSPPPWNEQE ETGSPFR TEN FSWDTLIEMP RSETTTMQFD SSNFGSYDFE
176 : -----

262 : DDVSFPSIWD YYGSLD
176 : -----RY
  
```

+++++

Sequence 1 : DREB2G.aa  
Size : 306  
Matching Position : 1 - 306

Sequence 2 : DREB2H.aa  
Size : 177  
Matching Position : 1 - 177

Matching Condition.

Matches : -1  
Mismatches : 1  
Gaps : 1  
\*N+ : 2  
  
Matching : 24.41 [%]  
Weight : 192

Fig. 5-20

```

                                0056504
1 : ----- --EEEQ-----PP AKKRNMGSR KGCМКGКGGP
    ** * * *** *****
1 : MPRKRKSRGT RDVAEILRKW REYNEQTEAD SCIDGGGSKP IRKAPPKRSR KGCМКGКGGP

27 : ENATCTFRGV RQRTWGKWVA EIREPNRGTR LWLGTFTSV EAAMAYDEAA KKLYGHEAKL
    ** * ** ***** ** * ** * ** *
61 : ENGICDYTG V RQRTWGKWVA EIREPGRGAK LWLGTFSY EAALAYDEAS KAIYGQSARL

87 : NLVHPQQQQ VVVNRNLSFS GHGSGSWAYN KKLDMVHGLD LGLGQASCSR GSCSERSSFL
    ** * *
121 : NL-----PL LPLCQA-----

147 : QEDDDHSHNR CSSSSGSNLC WLLPKQSDSQ DQETVNATTS YGGEGGGGST LTFSTNLKPK
    * * ***
131 : -----RL LHFLMNLKFV

207 : NLMSQNYGLY NGAWSRFLVG QEKKTEHDVS SSCGSSDNKE SMLVPSCGGE RMHRPELEER
    * * ** * * *
143 : HVRIQMQL- -----VLV- -----RSLTSRISK- -MLSP-----

267 : TGYLEMDDL EIDDLGLLIG KNGDFKNWCC EEFQHPWNWF
    * * *
168 : -----ITALVKL-----GRY

```

Fig. 6

DREB1C.nuc 1:ATGAACCTCATTTT...CTGCCCTTTTCTGAAATGTTT...GGCTCCGATTACGAGTCTCCGCTTTCCTCGGCCGGTGGATTACA  
DREB1D.nuc 1:ATGAATCCATTTTACTCTACATTCCTGAGCTCGTTTCTCTCAATCTCCGATCATAGATCTCCGCTTTCAGACAGTACTGAGTGT  
DREB1A.nuc 1:ATGAACCTCATTTT...CTGCCCTTTTCTGAAATGTTT...GGCTCCGATTACGAGTCTCCGCTTTCCTCGGCCGGTGGATTACA  
DREB1B.nuc 1:ATGAACCTCATTTT...CTGCCCTTTTCTGAAATGTTT...GGCTCCGATTACGAGTCTCCGCTTTCCTCGGCCGGTGGATTACA  
DREB1E.nuc 1:.....ATGCAAAACGAGC  
DREB1F.nuc 1:.....ATGAATAATGATG

DREB1C.nuc 77:GTCGGAAGCTTGCCACGAGCTGCCCGAGAAACACGCGGGAAGGAAGAAGTTTCGTGAGTCTCGTCACCCCAATTACAGAGGAGT  
DREB1D.nuc 86:CACCAAAAGTTAGCTTCTACGTCTGCCAAGAAACGAGCTGGGAGGAAGAAGTTTCGTGAGTCACTCGTCATCCGATTACAGAGGAGT  
DREB1A.nuc 77:GTCGGAAGCTTGCCACGAGCTGCCCGAGAAACGAGCTGGGAGGAAGAAGTTTCGTGAGTCACTCGTCATCCGATTACAGAGGAGT  
DREB1B.nuc 68:GTCGGAAGCTTGCCACGAGCTGCCCGAGAAACGAGCTGGGAGGAAGAAGTTTCGTGAGTCACTCGTCATCCGATTACAGAGGAGT  
DREB1E.nuc 14:ATATCACCGTGGCCAGGATGAAAGCCAAAGAAAGCTCCTGGACGGAGGATTTTCAAGGAGACACGTCAACCAATTTACAGAGGAGT  
DREB1F.nuc 14:ATATTATTCTGGCGGAGATGAGGCTTAAGAAAGCTCCTGGGAGGAGAGTCTTTAAGGAGACACGTCAACCAATTTACAGAGGAGT

DREB1C.nuc 162:TCGTCAGAGAACTCCGGTAAAGTGGGTGTGTGAGTTGAGAGAGCCAAACAAGAAACGAGGATTTGGCTCGGGACTTTCCAAACCC  
DREB1D.nuc 171:TCGTCAGAGAACTCCGGTAAAGTGGGTGTGTGAGTTGAGAGAGCCAAACAAGAAACGAGGATTTGGCTCGGGACTTTCCAAACCC  
DREB1A.nuc 162:TCGTCAGAGAACTCCGGTAAAGTGGGTGTGTGAGTTGAGAGAGCCAAACAAGAAACGAGGATTTGGCTCGGGACTTTCCAAACCC  
DREB1B.nuc 153:TCGTCAGAGAACTCCGGTAAAGTGGGTGTGTGAGTTGAGAGAGCCAAACAAGAAACGAGGATTTGGCTCGGGACTTTCCAAACCC  
DREB1E.nuc 99:GCGGCTAGCGGACGGCCACAAATGGGTATGCGAAGTCCGTGAACCGATTTCATCCGCTCGAGTCTGGCTCGGGACTTTCCAAACCC  
DREB1F.nuc 99:AAAGCGGAGGACGGTGAACAATGGGTCTCGGAAGTACAGAAACCGACGACCAACGCGCCATTGGCTCGGGACTTTCCAAACCC

DREB1C.nuc 247:GCTGAGATGGCAGCTCGTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGCAATCTGCTGTCTCAATTTCCGTGACTCGGGCTT  
DREB1D.nuc 256:GTCGAAATGGCTGCTCCTGCTCATGATGCTGCTGCTTTAGCTCTCGTGGTCTGCTCTGCTCTCAATTTCCGTGACTCGGGCTT  
DREB1A.nuc 247:GCTGAGATGGCAGCTCGAGCTCAGGAGCTGCCGCCATAGCTCTCGTGGTCTGCTCTGCTCTCAATTTCCGTGACTCGGGCTT  
DREB1B.nuc 238:GCTGAGATGGCAGCTCGTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGTCTGCTCTGCTCTCAATTTCCGTGACTCGGGCTT  
DREB1E.nuc 184:GCAGATATGGCAGCGCTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGTCTGCTCTGCTCTCAATTTCCGTGACTCGGGCTT  
DREB1F.nuc 184:GCAGATATGGCAGCGCTGCTCAGGAGCTGCCGCCATAGCTCTCGTGGTCTGCTCTGCTCTCAATTTCCGTGACTCGGGCTT

DREB1C.nuc 332:GGCGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGCTGAAGCCGCGTGAATTTTCAA...GATGAG  
DREB1D.nuc 341:GGCGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGCTGAAGCCGCGTGAATTTTCAA...GATGAG  
DREB1A.nuc 332:GGCGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGCTGAAGCCGCGTGAATTTTCAA...GATGAG  
DREB1B.nuc 323:GGCGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGCTGAAGCCGCGTGAATTTTCAA...GATGAG  
DREB1E.nuc 269:GGAGGTTGCGCGGTGCGCGGCTACCTGATCCGACACGATCAGGCGGCGCGCGGCTGAAGCCGCGTGAATTTTCAA...GATGAG  
DREB1F.nuc 269:GGCGGCTACGAATCCCGGAATCAACCTGTGCCAAGGAATCCAAAGCGCGCGGCTGAAGCCGCGTGAATTTTCAA...GATGAG

DREB1C.nuc 415:AT...GTGTCATTCAGCAAGGATGCTCATGCTCTTACATGGAGGA...GACCTTGGTGGAGGCT...ATTTATA  
DREB1D.nuc 424:ATACGACGAGGAGGATCTAAACTGCGGCGGAGGCGAGAGGAGGCGGAGGAGGAGG...GTGAGGAGGAGGAG...AGGAGGG  
DREB1A.nuc 415:AT...GTGTCATTCAGCAAGGATGCTCATGCTCTTACATGGAGGA...GACCTTGGTGGAGGCT...ATTTATA  
DREB1B.nuc 406:AT...GTGTCATTCAGCAAGGATGCTCATGCTCTTACATGGAGGA...GACCTTGGTGGAGGCT...ATTTATA  
DREB1E.nuc 354:GTT...AGTACAGGATATACGTTTACCTCAGCCAGTGA...TTTACACG...  
DREB1F.nuc 354:TTTA...GAAAGTGGAATTACGTTTTCCTTCTGCGGGAGATGATGTTGATTGCTTTTGGTTCGGGTCCGCGCTCTG

DREB1C.nuc 482:CGCCGGAAC...AGAGCCAGATGCGGTTTATATGGATGAAGAGGCGATGTTGGGATGCTTAGTGTGTTGGATAACATGGCCG  
DREB1D.nuc 503:CGGAGGAGC...AGAATGCTGCTGTTTATATGGATGAAGAGGCGATGTTGGGATGCTTAGTGTGTTGGATAACATGGCCG  
DREB1A.nuc 479:CGCCGGAAC...AGAGCCAGATGCGGTTTATATGGATGAAGAGGCGATGTTGGGATGCTTAGTGTGTTGGATAACATGGCCG  
DREB1B.nuc 473:CGCCGGAAC...AGAGCCAGATGCGGTTTATATGGATGAAGAGGCGATGTTGGGATGCTTAGTGTGTTGGATAACATGGCCG  
DREB1E.nuc 402:TCGG...ATGAAGGAGTCCGTCGATGATGATGATGAGGCTCGCGG  
DREB1F.nuc 431:GTTCCGGATCGGAGGAGAGGATCTCTCTTCGATGGATTGAGAGTACCAAGAGTCTCAGCAGCATGATGAGACTCGCGG

DREB1C.nuc 563:AGGGATGCTTTTACCGTCCGC...GTCGGTCAATGGAACTATAATT...TTGATGTCGAGGGAGA...TGATGA  
DREB1D.nuc 584:AGGGATGCTTTTACCGTCCGC...GGAAGTGGCTGGAATCATAAC...GACTTTCAGGAGT...GGGTGA  
DREB1A.nuc 560:AGGGATGCTTTTACCGTCCGC...GTCGGTCAATGGAACTATAATT...TTGATGTCGAGGGAGA...TGATGA  
DREB1B.nuc 554:AGGGATGCTTTTACCGTCCGC...GTCGGTCAATGGAACTATAATT...TTGATGTCGAGGGAGA...TGATGA  
DREB1E.nuc 443:AGGAGCCGTTGATGTCGCGGCAAGATCGTACATTGA...TATGAT...ACGAGTGTGATGCTGAGGAGGAGA...TGGTGA  
DREB1F.nuc 515:AGGGCCACTAATGTCGCGGCGCGGATCGTATATGGAGAGCATGACCTACTAATGTTTACAGGAGAGAGATGCTGTTATGA

DREB1C.nuc 630:CG...TGTCCTTATGGAGCTATTA...  
DREB1D.nuc 648:CG...TGTCCTTATGGAGCTATTA...  
DREB1A.nuc 627:CGAGCTATCGTTATGGAGTTATTA...  
DREB1B.nuc 621:CG...TGTCCTTATGGAGTTATTA...  
DREB1E.nuc 522:AGATTGTCTACTTGGAGTTATTA...  
DREB1F.nuc 600:AGATATGTCATGTTGGAGTTACAGATATTA

DREB2A.nuc  
DREB2B.nuc  
DREB2C.nuc  
DREB2H.nuc  
DREB2E.nuc  
DREB2D.nuc  
DREB2G.nuc  
DREB2F.nuc

[illegible]

DREB2A.nuc  
DREB2B.nuc  
DREB2C.nuc  
DREB2D.nuc  
DREB2E.nuc  
DREB2F.nuc  
DREB2G.nuc  
DREB2H.nuc  
DREB2I.nuc  
DREB2J.nuc  
DREB2K.nuc  
DREB2L.nuc  
DREB2M.nuc  
DREB2N.nuc  
DREB2O.nuc  
DREB2P.nuc  
DREB2Q.nuc  
DREB2R.nuc  
DREB2S.nuc  
DREB2T.nuc  
DREB2U.nuc  
DREB2V.nuc  
DREB2W.nuc  
DREB2X.nuc  
DREB2Y.nuc  
DREB2Z.nuc

DREB2A. nuc 159 GAA ..... AGTAACTCTGGAAGGCTGCGAA GAA GGGTTGTT TGAAGGCTGAAGGA GGAACCAAGAGATTAAGCCGAT  
 145 CAA ..... GGAA CCGAAGACGCTACTCTCTGCAAAAGC TCGGA GAAAGTTGTGTT TGAAGGCTGAAGGA GGAACAGATTAATTCCTACAT  
 124 GGTCCCAAA TGAAT TCGAAGGCTTCCCTCTTAAGCTTCGAG GAAAGGTTGTGTT TGAAGGCTGAAGGCTGCACTTGA AAA CCGGATTT  
 109 GGTCTCAAA CAAAT TCGAAGGCTTCCCTCTTAAGCTTCGAG GAAAGGTTGTGTT TGAAGGCTGAAGGCTGCACTTGA AAA CCGGATTT  
 118 GATTGGCGAAGCTCTGTGGCTTCAAGTCCAAAGCTTCGAG GAAAGGTTGTGTT TGAAGGCTGAAGGCTGCACTTGA AAA CCGGATTT  
 45 GAA ..... TACCAAGCAAGCC ..... GTACGCAAGAA GAAAGGTTGTGTT TGAAGGCTGAAGGCTGCACTTGA AAA CCGGATTT  
 10 GAGCAACCTCTCGCGCAAGAACCAACATGCGGA GAAAGCTTGAAGGCTGAAGGCTGCACTTGA AAA CCGGATTT  
 1: ..... ATGGAGAAATGATCTCTGATATGAGGAA GAAAGCTTGAAGGCTGAAGGCTGCACTTGA AAA CCGGATTT

230 **GTAGTT** **CAGAGGAGTATGACAAAGGATTTGGGGTAAATGGGTGTGAGATCA** **CA** **GAGCCTA** ..... **ATC** **GAGGTA** **GCA** .....  
 227 **GTAGTT** **ACAGGAGTTAGACA** **AAAGCATTTGGGTAAATGGGTGTGACAGATCA** **CA** **GAGCCTA** ..... **AAATAGGAA** **GTA** .....  
 209 **GTAGCTAT** **ACAGGAGTTAGACA** **GAGGATGGGTAAATGGGTGTGAGAT** **CCGTGAGCCAG** ..... **ACG** **GAGGTGCTA** .....  
 194 **GTGACATA** **ACAGGAGTTAGACA** **GAGGATGGGTAAATGGGTGTGAGAT** **CCGTGAGCCAG** ..... **GCC** **GAGGTGCTA** .....  
 203 **CTCGGTT** **TAGAGTGTTCGACA** **AAAGCCTTGGCCAAATGGGTGTGAGAT** **ACGTGATCA** **CCGTGAGGCA** **ACTC** .....  
 119 **GCCTCT** **TACAGAGTGTTCGACA** **AAAGCCTTGGCCAAATGGGTGTGAGAT** **CCGTGAGGCTA** ..... **ACCGAGGAG** **ACTC** .....  
 95 **GTACTCT** **CTCGGAGTTAGACA** **CGGACTTGGGTAAATGGGTGTGAGAT** **CCGTGAGCCTA** ..... **ACCGTGGGA** **ACTC** .....  
 77 **GTCAAGTAC** **CGTGGAGTACG** **CAAGGACTTGGCCAAATGGGTGTGAGAT** **CNCTGAGCCCA** ..... **AGAAGGAGGCA** .....

[illegible]

376 **TATGGTCTTATGGCTCGTCTTAATTTCGC** ..... **TGGTCWGTGATGCGTCT**... **GAGTAAAGAGTAACTCTCAAGTCACT**  
 373 **TACGGTTCATGGCTCGTCTTAATCTTCGC** ..... **TGAGTCTGTGGTCT**... **GAGTAACTAGTACGCTAGTCAAT**  
 355 **TACGGTTCAGCTGCGAGATCAATCTTCG** ..... **CGAGATCACAAAATGCGCTCTCTTC**... **CGAGTCTGCCATCCACTGCTAGTCACTCGG**  
 340 **TACGGTTCAGCTGCGCGGCAATCTTC** ..... **ACTGCTGCGCATGCTCAGGCTCGG**  
 373 **TACGGCATGCTGCGGAGTAAATTCGCT** ..... **ATGCTGCTGCTGCTGCTGCTGCTCGG**  
 265 **TATGGCTGCTGCTGCTGCTGCTGCTGCTGCT** ..... **GAGATGCTGGTGGGGAAGAGTAA**  
 241 **TATGGCATCAGGAGCTAAATCTCAA** **CTGGTGCACC**... **AGAACCAACAACAAGTAGTACGAGAGAACTTACCTCAAA**  
 223 **TATGGGATCGATACCTCAATTAAGCTC** ..... **ATCTTCAGCGGAATACAGACTTCTCTGAGTCACTATCAG**

445-CTGACGCTGTTACCTGAGA.....CTCCGGGTTCTGTCATGCGAATAACAGAGGATCCCTGGATTGCAATCTTAAAAAC  
 443-CTCAGCGCTGTACCGTTCAGTAAGCTGCTGCTGAAGTTGTGCTGCAAGCATGAGATCTCTGGTGAATCAATAATCC  
 440-TTATCTGATCTTCTGACAA.....TCTGAACTATAGTGCCTCCAGAGGTATACAAATGCGAAGTTCAAGTTCAGTAATCC  
 394-TTACTCATCTTCTGACAA.....TCTGCAAGTTCGAGCGGATACAAATGCAAGATCTGGTTCTGCTGCA  
 428-ACGACGAGGAGGCGGAAG.....TCTGGAGGCTGATGGGTTCGAAATAATCAACAGCGGTAATCCCTGCTGCTCA  
 319-ACGGCGCTCTCTCGGGT.....CCGACAGTACACCTAGCAAGAGCCGCGGCGGGAATAACGACGAGGACTC  
 320-CTGGCGACGGGCGGCTCTGG.....GCTTAATAAAGAAAGCTGATATGGTTCATGGGTGGACCTTGGCTCTGGCCCA  
 295-AGGCTTCAATGGGTACCTTCAGGAAGTTTATATGTAAGTTCCTTCATGCTGGTATGCTTAAACGTGTGACAGCCCAATGCT



Fig. 7-2

[illegible]

Fig. 8

DREB1A 1:...MNSFSAFSEMFSGDYESSVSSGGDYIPTLASSCPKKRGRKKKPRETRHPPIYRGVRR  
DREB1B 1:...MNSPFAFSEMFSGDYEP...QGGDYCPFLATSCPKKPAGRKKPRETRHPPIYRGVRR  
DREB1C 1:...MNSPFAFSEMFSGDYESPVSSEKLAATSCPKKPAGRKKPRETRHPPIYRGVRR  
DREB1D 1:MNPPYSTPPDSFLSISDHRSPVSDSSKSPKASSCPKPAGRKKPRETRHPPIYRGVRR  
DREB1E 1:.....NENDITVAEMKPKKPAGRKKPRETRHPPIYRGVRR  
DREB1F 1:.....MNNDDITLAEKMPKKKPAGRKKPRETRHPPIYRGVRR

DREB1A 57:RNSGKNVCEVREPKKTRINLCTFTAEAAARAHDVAALALGRSACLNFADSAVRLRI  
DREB1B 54:RNSGKNVSEVREPKKTRINLCTFTAEAAARAHDVAALALGRSACLNFADSAVRLRI  
DREB1C 57:RNSGKNVCEVREPKKTRINLCTFTAEAAARAHDVAALALGRSACLNFADSAVRLRI  
DREB1D 60:RNSGKNVCEVREPKKTRINLCTFTAEAAARAHDVAALALGRSACLNFADSAVRLRI  
DREB1E 36:RQDKNVCEVREETHQRRVILCTFTADAAARAHDVAALALGRSACLNFADSAVRLPV  
DREB1F 36:RNSGKNVCEVREETHQRRVILCTFTADAAARAHDVAALALGRSACLNFADSAVRLPV

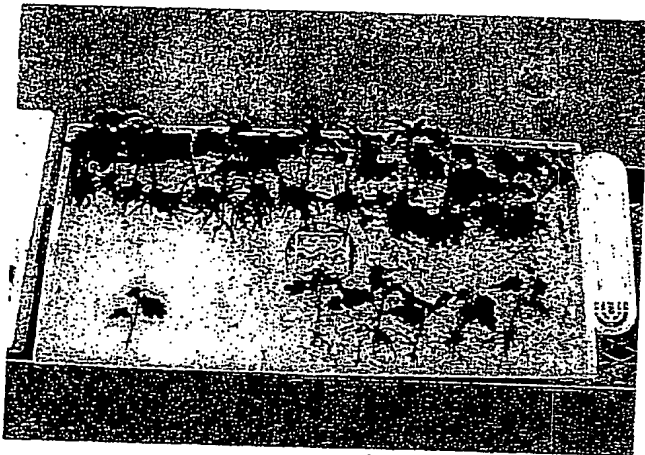
DREB1A 116:PESTCAKDIOKAAAEHALAFQDEMCDATDTHG.FDNEZNLVEAIYTAE.....QSENAF  
DREB1B 113:PESTCAKDIOKAAAEHALAFQDETCDTTTNEGLDNEETNVEAIYTPE.....QSEGAR  
DREB1C 116:PESTCAKDIOKAAAEHALNFQDEMCHMTDAGLDNEETNVEAIYTPE.....QSEODAF  
DREB1D 119:PEETCPKSIOKAASBAAMACNETTEGSKTA.AEAEBAAGCGVREGGRRAEEQNGGVF  
DREB1E 95:PASTDPTDTRHTAASAAEMGRPPFPSTGTVLPASAEFDT.....  
DREB1F 95:PESTDPTDTRHTAASAAEMGRPPVLESGITVLPACGDDVDLGFSGSGSGSGSEERNSS

DREB1A 169:NMDEEAMPENPSSLANMAEGMLLPSPSQNNHH.....EVDGDDDVSLMSY..  
DREB1B 167:NMDEETMFGPTLLDNNAEGLLPSPSQNNHHY.....DGECDGVSLMSY..  
DREB1C 170:NMDEEAVLGSSLLDNNAEGLLPSPSQNNYF.....DVEGDDDVSLMSY..  
DREB1D 177:NMDEEALLGPNPFENNAEGMLLPSPSQNNH.....DFDGVCDVSLMSFDE  
DREB1E 135:.....DEGVAGNMRLAEFPMSPSRYIDNM..TSVVDESMCYEDISLMSY..  
DREB1F 154:SYGFGDYEEVSTTMRLAEGFMSPSRYMEDNTPTNVYTEEMCYEDISLMSYRY

Fig. 9

DREB2A 1:MAVYDQSGDRNRTOIDTSRRKRSRSGDGTVAERKKRKKYNEITVSEVSTK.....KRVVPAKSGKKGCKNKGKGG  
DREB2B 1:MAVVEQTG.....TEQPKRKSRARAGGLTVADREKKKKYNEIVEASAVKEG...EKP KRVVPAKSGKKGCKNKGKGG  
DREB2C 1:MPSE.....IVDRKRSR...GTRDVAEIRQVREYNEQIEAESCIDGGEPKSIKPPPKESRKGCARGKGG  
DREB2D 1:.....MEKEDNGSKQSSASUVSSRRRRRVVEPVEATLQWEEEGLARARRVQA KSGKKGCKNKGKGG  
DREB2E 1:.....MEKSSSSKQ.....MEKSSSSKQ.....WKGPARGKGG  
DREB2F 1:.....MEEEQPPAKRRNNGRSRKGCNKGKGG  
DREB2G 1:MP.....GTRDVAEIRKRWREYNEQTEADSCIDGGGSKPIRKAPPKRSRKGCNKGKGG  
DREB2H 1:MP.....RKRKSR...GTRDVAEIRKRWREYNEQTEADSCIDGGGSKPIRKAPPKRSRKGCNKGKGG  
DREB2A 72:PERISGCFRGVRORIMOKWVAEIREPN.....RGSRLNLGTFPTAQEASASAYDEAAKAMYGPLARLNPFRSD...  
DREB2B 71:PDNSHCFSRGVRORIMOKWVAEIREPK.....IGRLNLGTFPTAERASAYDEAATAMYGSLARLNPQSV...  
DREB2C 65:PENGICDYRGVRORIMOKWVAEIREPD.....GRLNLGTFSSSYEAALAYDEAAKAIWQ SARLNLPEITNRS  
DREB2D 35:PDNASCTYKRGVRORTGKVAEIREPN.....RGRNLGTFPTSRERAAALAYDSAR KLYGPBARLNLPESLR...  
DREB2E 63:PERPVCRRFRGVRORTGKVAEIREPVSHRGANSRKRRLNLGTFATAEAALAYDRAASVMKGPYARLNPEDLG...  
DREB2F 21:PQNALCOYRGVRORTGKVAEIREPK.....KRALNLGTFATAEAALAYDEAAL KLKCHDAYLNEPHLQRN...  
DREB2G 27:PENATCTFRGVRORTGKVAEIREPN.....RGRNLGTFPTSVAAAMAYDEAAK KLYGHEAKLNLVHPQOQ...  
DREB2H 60:PENGICDYTCVRORTGKVAEIREPG.....RGAKNLNLGTFSSSYEAALAYDEASKAIYGO SARLNLPLP...  
DREB2A 138:.....ASEVSTSSQSEVCTVETPGCVH...VKTEBDDCESKPPSG...GVEPMYCLN.....GAHEHKGUV  
DREB2B 137:.....GSEFTSTSSQSEVCTVENKAVCGDVCKKHEDTDCESNPFQILDVREESCCTRPDSCVGHQDMNSSL  
DREB2C 135:SS TAATA TVSGSVTAPSESEVCAREDTNASSGFGVUKLEDSCDEYLLDSSQICKELKXEE...VREHNLA V  
DREB2D 102:.....SYPKTASSPASQTTPS  
DREB2E 138:.....GGRKXDEEAESSGYWLETNKAGNGVETEG...GKDYVVYN.....  
DREB2F 89:.....TRPSLSNSORFKWVPSR...XPFISMPSCGMLNVAQPSVHI IQORLEELKXKTGL  
DREB2G 95:.....QOVVUNRNLSFGSGSGSWAYNKKLDVHGLDGLGQASC SRGSCSERSFLQEDDD  
DREB2H 126:.....LQOARLLHFLMLNLFVHVRIOMQDLVLVRS...LTSR.....  
DREB2A 196:KADKHWLSEFEHNYWSDILKEKX...QKEQGIVETCQQQQQ.....DSMSVADYGP..NDV..DQSHLDS...SDM  
DREB2B 207:NYD...LLEFEQYWGQVLQEKEXKPKOEESIQQQQQQQQQQLOPDLITVADYGPWNSNDIVNDQTSWDP...NEC  
DREB2C 208:GFG...IGQDSKRETLDAWLMGNGNEQEPLEFGVDETFD..INELGILNDDNNVSGQETMQYQVDRHPNFSYQTQ  
DREB2D 118:..SNTGCKSSSDS.....ESPCSS...NEMSSCG.....RVTEEISWEHINVDLPVMD...S  
DREB2E 177:.....ESKXNTSFLDEKTSKGETDNMFEGGQKKPEIDLTEFLQGLILKDN.....SA  
DREB2F 142:LSQSYSSSSST.....ESKXNTSFLDEKTSKGETDNMFEGGQKKPEIDLTEFLQGLILKDN.....SA  
DREB2G 153:HSNRCSSSSGSNLCWLLPKQSDSQDETUNATSYGEGGGGSTLFTSTNLKPKNLMSQNYGLYNGAWSRPLVGQSK  
DREB2H 160:.....ISKMSPI.....TALVKLGRY.....  
DREB2A 259:FDVDELLRDNGDDVFAGLNQDRYPGNSVANGSYRPESQQSGDFDPLQSLNYGIPPPQLEGKXGNGFFFDLSYLDLEN  
DREB2B 279:FDINELLGDN.....EPGPHQSQDQ...NHVNSGSYDLPLHLEPHDG.HEPNGLSSLDI..  
DREB2C 278:FPNSNLLGSN.....PNEIAQPGVDYCPYVQPSDMENYIGIDLHRRFNDLIDQLDQDGGCKDVHGST...  
DREB2D 164:SIWEEATMSGPPWVHEGDN.....DISR.....FDTGISGGY.....SNWDSFHSPL...  
DREB2E 208:YSYDRFK.....LDNGLLYNEPQSSSYHQGGGFDSEYEFPRF.....  
DREB2F 204:EPSEVAECHSPPPWNQOETGSPFRTENPFWDTLIEMPRSETTMQFDSSNFGSYDFEDDVSPFSIWQYIGSLD...  
DREB2G 231:KTEHDVSSCGSSDNKESMLVPSGGERMHRPELEERTGYLEMDDLEIDDLGLLIGKNGDFKXNCCERFQHPWNWP  
DREB2H :.....

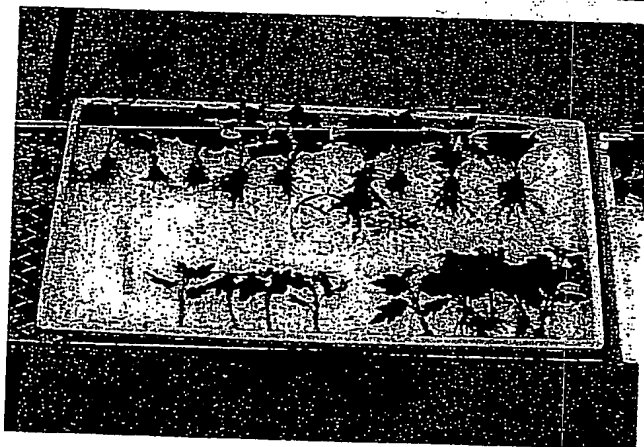
Fig. 10



strain 9



strain 10



non-transformant

Fig. 11

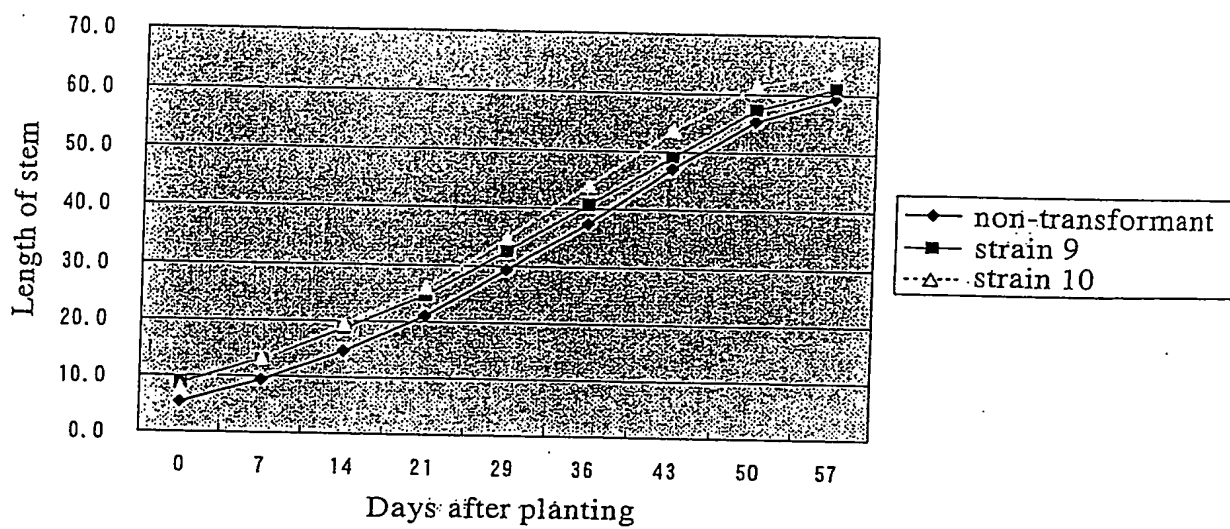
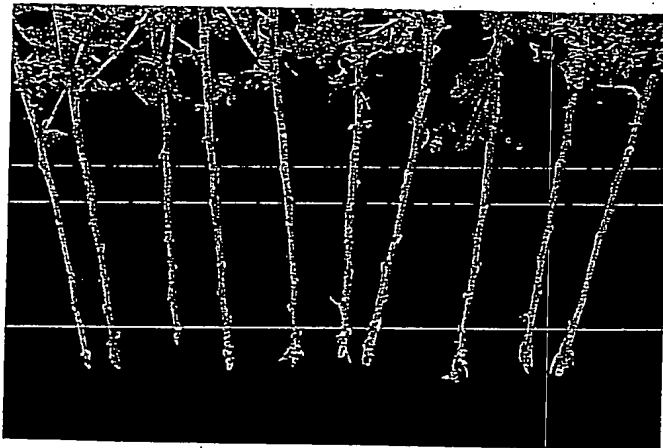


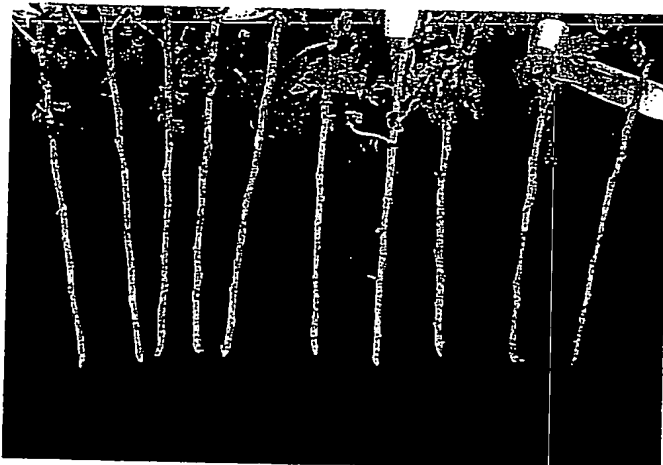
Fig. 12



strain 9



strain 10



non-transformant